1) CORE OVER ... ACCESS DB # 180964

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Scientific and Technical Information Center

SEARCH REQUEST FORM

10/719,370

Requester's Full Name: JANE ZARA Examiner #: 7757 Date: 5/24/06

Art Unit: 1635 Phone Number: 2-0765 Serial Number: [redacted]

Location (Bldg/Room#): 2D28 (Mailbox #): 2C18 Results Format Preferred (circle): PAPER DISK

****

To ensure an efficient and quality search, please attach a copy of the cover sheet, claims, and abstract or fill out the following:

Title of Invention: Modulation of HIF 1 α

Inventors (please provide full names): D T Ward et al.

Earliest Priority Date: 11/21/03

Search Topic:

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc., if known.

For Sequence Searches Only *Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.*

20 NA

Please Search Seq ID No: 446

- Length limits better 18 - 50 NTS. 12 - 50 NTS
- 70% Homology or greater
- Score over Length search
- No interference data bases.

RECEIVED MAY 24 2006 BIOTECH/BIOINFO (STIC)

****

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Searcher: Jan

Searcher Phone #: 72504

Searcher Location: _____

Date Searcher Picked Up: 6/6/06

Date Completed: 6/13/06

Searcher Prep & Review Time: 15

Online Time: 45

Type of Search

✓ NA Sequence (#)

___ AA Sequence (#)

___ Structure (#)

___ Bibliographic

___ Litigation

___ Fulltext

___ Other

Vendors and cost where applicable

___ STN ___ Dialog

___ Questel/Orbit ___ Lexis/Nexis

___ Westlaw ___ WWW/Internet

✓ In-house sequence systems

✓ Commercial ___ Oligomer ✓ Score/Length

___ Interference ___ SPDI ___ Encode/Transl

___ Other (specify)

GenCore version 5.1.9

OM nucleic - nucleic search, using sw model

Run on: June 13, 2006, 15:51:49 ; Search time 0.001 Seconds
(without alignments)
12.960 Million cell updates/sec

Title: US-10-719-370A-446
Perfect score: 20
Sequence: 1 cctcatggtcacatggatga 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 0.5

Searched: 25 seqs, 324 residues

Total number of hits satisfying chosen parameters: 50

Minimum DB seq length: 12
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 25 summaries

Database : us-10-719-370a-446.sl.rni4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	14.8	74.0	19	1	US-08-846-020A-22	Sequence 22, Appl
2	14.8	74.0	19	1	US-09-617-871-22	Sequence 22, Appl
c 3	12.2	61.0	17	1	US-09-866-108A-7612	Sequence 7612, Ap
4	10.8	54.0	15	1	US-09-081-646-513	Sequence 513, App
5	9.4	47.0	13	1	US-09-374-704-12	Sequence 12, Appl
c 6	9.4	47.0	13	1	US-09-374-704-13	Sequence 13, Appl
c 7	9	45.0	12	1	US-08-441-887A-200	Sequence 200, App
c 8	8.4	42.0	12	1	US-08-030-335-10	Sequence 10, Appl
c 9	8.4	42.0	12	1	US-07-973-431B-3	Sequence 3, Appli
c 10	8.4	42.0	12	1	US-08-122-433-26	Sequence 26, Appl
c 11	8.4	42.0	12	1	US-08-623-891-24	Sequence 24, Appl
c 12	8.4	42.0	12	1	US-08-480-020B-10	Sequence 10, Appl
c 13	8.4	42.0	12	1	US-08-910-618-10	Sequence 10, Appl
c 14	8.4	42.0	12	1	US-09-105-515-2	Sequence 2, Appli
c 15	8.4	42.0	12	1	US-08-910-322-10	Sequence 10, Appl
c 16	8.4	42.0	12	1	US-08-679-493A-68	Sequence 68, Appl
c 17	8.4	42.0	12	1	US-08-484-939A-10	Sequence 10, Appl
c 18	8.4	42.0	12	1	US-09-340-861-24	Sequence 24, Appl
c 19	8.4	42.0	12	1	US-09-634-262-24	Sequence 24, Appl
c 20	8.4	42.0	12	1	US-09-748-044-2	Sequence 2, Appli
c 21	8.4	42.0	12	1	US-09-384-472-10	Sequence 10, Appl
22	8.4	42.0	12	1	US-09-835-370-54	Sequence 54, Appl
23	8.4	42.0	12	1	US-09-793-146-38	Sequence 38, Appl
24	8.4	42.0	12	1	US-09-793-146-48	Sequence 48, Appl
c 25	8.4	42.0	12	1	US-09-793-146-49	Sequence 49, Appl

ALIGNMENTS

RESULT 1
US-08-846-020A-22
; Sequence 22, Application US/08846020A
; Patent No. 6090547
; GENERAL INFORMATION:
; APPLICANT: Drazen M.D., Jeffrey M.
; APPLICANT: In M.D., Kwang-Ho
; APPLICANT: Asano M.D., Koichiro
; APPLICANT: Beier, David
; APPLICANT: Grobholz, James
; TITLE OF INVENTION: 5-Lipoxygenase Gene Sequence
; TITLE OF INVENTION: Polymorphisms and Their Use in Classifying Patients
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CHOATE, HALL & STEWART
; STREET: 53 State Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109-2891
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/846,020A
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Jarrell Ph.D., Brenda H.
; REGISTRATION NUMBER: 39,223
; REFERENCE/DOCKET NUMBER: 0092662-0012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 248-5000
; TELEFAX: (617) 248 4000
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "primer"
; IMMEDIATE SOURCE:
; CLONE: Exon 4 sense primer
US-08-846-020A-22

Query Match 74.0%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred. No. 0.91;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy          2 CTCATGGTCACATGGATG 19
              |||||| ||| |||||||
Db          2 CTCATGCTCAGATGGATG 19
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RESULT 2
US-09-617-871-22
; Sequence 22, Application US/09617871
; Patent No. 6355434
; GENERAL INFORMATION:
; APPLICANT: Drazen M.D., Jeffrey M.
; APPLICANT: In M.D., Kwang-Ho
; APPLICANT: Asano M.D., Koichiro
; APPLICANT: Beier, David
; APPLICANT: Grobholz, James
; TITLE OF INVENTION: 5-Lipoxygenase Gene Sequence
; TITLE OF INVENTION: Polymorphisms and Their Use in Classifying Patients
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CHOATE, HALL & STEWART
; STREET: 53 State Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA

```
;       ZIP:  02109-2891
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.30
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/09/617,871
;       FILING DATE:
;       CLASSIFICATION:
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  08/846,020
;       FILING DATE:
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Jarrell Ph.D., Brenda H.
;       REGISTRATION NUMBER:  39,223
;       REFERENCE/DOCKET NUMBER:  0092662-0012
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (617) 248-5000
;       TELEFAX:  (617) 248 4000
;   INFORMATION FOR SEQ ID NO:  22:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  19 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  other nucleic acid
;       DESCRIPTION:  /desc = "primer"
;     IMMEDIATE SOURCE:
;       CLONE:  Exon 4 sense primer
US-09-617-871-22

  Query Match             74.0%;  Score 14.8;  DB 1;  Length 19;
  Best Local Similarity   88.9%;  Pred. No. 0.91;
  Matches   16;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 CTCATGGTCACATGGATG 19
              |||||| ||| |||||||
Db          2 CTCATGCTCAGATGGATG 19


RESULT 3
US-09-866-108A-7612/c
; Sequence 7612, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
;  APPLICANT: GU, Yizhong
;  APPLICANT:  JI, Yonggang
;  APPLICANT:  PENN, Sharron G.
;  APPLICANT:  HANZEL, David K.
;  APPLICANT:  RANK, David R.
;  APPLICANT:  CHEN, Wensheng
;  APPLICANT:  SHANNON, Mark
;  TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
;  FILE REFERENCE: AEOMICA-7
;  CURRENT APPLICATION NUMBER: US/09/866,108A
;  CURRENT FILING DATE:  2001-05-25
;  PRIOR APPLICATION NUMBER: US 60/207,456
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: GB 24263.6
;  PRIOR FILING DATE: 2000-10-04
;  PRIOR APPLICATION NUMBER: US 60/236,359
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: PCT/US01/00666
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00667
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00664
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00669
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00665
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00668
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00663
;  PRIOR FILING DATE: 2001-01-30
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 15755
;  SOFTWARE: Aeomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 7612
;   LENGTH: 17
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-866-108A-7612

  Query Match             61.0%;  Score 12.2;  DB 1;  Length 17;
  Best Local Similarity   82.4%;  Pred. No. 2.8;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 CCTCATGGTCACATGGA 17
              ||||| ||||||| | |
Db         17 CCTCAAGGTCACAGGTA 1


RESULT 4
US-09-081-646-513
; Sequence 513, Application US/09081646
; Patent No. 6333152
; GENERAL INFORMATION:
;  APPLICANT: Kinzler, Kenneth
;  APPLICANT: Vogelstein, Bert
;  APPLICANT: Zhang, Lin
;  APPLICANT: Zhou, Wei
;  TITLE OF INVENTION: Gene Expression Profiles in No. 6333152mal and
;  TITLE OF INVENTION: Cancer Cells
;  FILE REFERENCE: 01107.74664
;  CURRENT APPLICATION NUMBER: US/09/081,646
;  CURRENT FILING DATE: 1998-05-20
;  EARLIER APPLICATION NUMBER: 60/047,352
;  EARLIER FILING DATE: 1997-05-21
;  NUMBER OF SEQ ID NOS: 871
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 513
;   LENGTH: 15
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-081-646-513

  Query Match             54.0%;  Score 10.8;  DB 1;  Length 15;
  Best Local Similarity   85.7%;  Pred. No. 4.4;
  Matches   12;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          4 CATGGTCACATGGA 17
              ||||| ||| ||||
Db          1 CATGGCCACGTGGA 14


RESULT 5
US-09-374-704-12
; Sequence 12, Application US/09374704
; Patent No. 6958240
; GENERAL INFORMATION:
;  APPLICANT: DERVAN, PETER B.
;  APPLICANT: BAIRD, ELDON J.
;  TITLE OF INVENTION: INHIBITION OF MAJOR GROOVE DNA BINDING
;  TITLE OF INVENTION: PROTEINS BY MODIFIED POLYAMIDES
;  FILE REFERENCE: 238/298
;  CURRENT APPLICATION NUMBER: US/09/374,704
;  CURRENT FILING DATE: 1999-08-12
;  EARLIER APPLICATION NUMBER: PCT/US98/02684
;  EARLIER FILING DATE: 1998-02-13
;  EARLIER APPLICATION NUMBER: PCT/US97/03332
;  EARLIER FILING DATE: 1997-02-20
;  EARLIER APPLICATION NUMBER: PCT/US97/12722
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;  EARLIER FILING DATE: 1997-07-21
;  EARLIER APPLICATION NUMBER: 60/038,384
;  EARLIER FILING DATE: 1997-02-14
;  EARLIER APPLICATION NUMBER: 60/023,309
;  EARLIER FILING DATE: 1996-07-31
;  EARLIER APPLICATION NUMBER: 60/024,374
;  EARLIER FILING DATE: 1996-08-01
;  EARLIER APPLICATION NUMBER: 60/026,713
;  EARLIER FILING DATE: 1996-09-25
;  EARLIER APPLICATION NUMBER: 08/853,522
;  EARLIER FILING DATE: 1997-05-08
;  EARLIER APPLICATION NUMBER: 08/837,524
;  EARLIER FILING DATE: 1997-04-21
;  EARLIER APPLICATION NUMBER: 08/607,078
;  EARLIER FILING DATE: 1996-02-26
;  NUMBER OF SEQ ID NOS: 20
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 12
;   LENGTH: 13
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: Polyamide Motif
US-09-374-704-12

  Query Match             47.0%;  Score 9.4;  DB 1;  Length 13;
  Best Local Similarity   90.9%;  Pred. No. 6.6;
  Matches   10;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 TCATGGTCACA 13
              ||||||||| |
Db          3 TCATGGTCATA 13


RESULT 6
US-09-374-704-13/c
; Sequence 13, Application US/09374704
; Patent No. 6958240
; GENERAL INFORMATION:
;  APPLICANT: DERVAN, PETER B.
;  APPLICANT: BAIRD, ELDON J.
;  TITLE OF INVENTION: INHIBITION OF MAJOR GROOVE DNA BINDING
;  TITLE OF INVENTION: PROTEINS BY MODIFIED POLYAMIDES
;  FILE REFERENCE: 238/298
;  CURRENT APPLICATION NUMBER: US/09/374,704
;  CURRENT FILING DATE: 1999-08-12
;  EARLIER APPLICATION NUMBER: PCT/US98/02684
;  EARLIER FILING DATE: 1998-02-13
;  EARLIER APPLICATION NUMBER: PCT/US97/03332
;  EARLIER FILING DATE: 1997-02-20
;  EARLIER APPLICATION NUMBER: PCT/US97/12722
;  EARLIER FILING DATE: 1997-07-21
;  EARLIER APPLICATION NUMBER: 60/038,384
;  EARLIER FILING DATE: 1997-02-14
;  EARLIER APPLICATION NUMBER: 60/023,309
;  EARLIER FILING DATE: 1996-07-31
;  EARLIER APPLICATION NUMBER: 60/024,374
;  EARLIER FILING DATE: 1996-08-01
;  EARLIER APPLICATION NUMBER: 60/026,713
;  EARLIER FILING DATE: 1996-09-25
;  EARLIER APPLICATION NUMBER: 08/853,522
;  EARLIER FILING DATE: 1997-05-08
;  EARLIER APPLICATION NUMBER: 08/837,524
;  EARLIER FILING DATE: 1997-04-21
;  EARLIER APPLICATION NUMBER: 08/607,078
;  EARLIER FILING DATE: 1996-02-26
;  NUMBER OF SEQ ID NOS: 20
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 13
;   LENGTH: 13
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: GCN4 binding molecule
US-09-374-704-13

  Query Match             47.0%;  Score 9.4;  DB 1;  Length 13;
  Best Local Similarity   90.9%;  Pred. No. 6.6;
  Matches   10;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 TCATGGTCACA 13
              ||||||||| |
Db         11 TCATGGTCATA 1


RESULT 7
US-08-441-887A-200/c
; Sequence 200, Application US/08441887A
; Patent No. 5837832
;  GENERAL INFORMATION:
;    APPLICANT:  Chee, Mark
;    APPLICANT:  Cronin, Maureen T.
;    APPLICANT:  Fodor, Stephen P.A.
;    APPLICANT:  Huang, Xiaohua X.
;    APPLICANT:  Hubbell, Earl A.
;    APPLICANT:  Lipshutz, Robert J.
;    APPLICANT:  Lobban, Peter E.
;    APPLICANT:  Morris, Macdonald S.
;    APPLICANT:  Sheldon, Edward L.
;    TITLE OF INVENTION:  Arrays of Nucleic Acid Probes on
;    TITLE OF INVENTION:  Biological Chips
;    NUMBER OF SEQUENCES:  360
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend and Crew LLP
;      STREET:  Two Embarcadero Center, 8th Floor
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94111
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/441,887A
;      FILING DATE:  16-MAY-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/143,312
;      FILING DATE:  26-OCT-1993
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/082,937
;      FILING DATE:  25-JUN-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Liebeschuetz, Joseph O.
;      REGISTRATION NUMBER:  37,505
;      REFERENCE/DOCKET NUMBER:  018547-004160US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  650-326-2400
;      TELEFAX:  650-326-2422
;  INFORMATION FOR SEQ ID NO:  200:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  12 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (probe)
US-08-441-887A-200

  Query Match             45.0%;  Score 9;  DB 1;  Length 12;
  Best Local Similarity   100.0%;  Pred. No. 6.8;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 CATGGATGA 20
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                ||||||||||
Db          11 CATGGATGA 3


RESULT 8
US-08-030-335-10/c
; Sequence 10, Application US/08030335
; Patent No. 5491073
;  GENERAL INFORMATION:
;    APPLICANT:  No. 5491073eborn, Matheus H
;    APPLICANT:  De Boer, Gerben F
;    TITLE OF INVENTION:  Cloning Of Chicken Anaemia DNA
;    NUMBER OF SEQUENCES:  11
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Cooper & Dunham
;      STREET:  30 Rockefeller Plaza
;      CITY:  New York, New York
;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  10112
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.24
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/030,335
;      FILING DATE:  08-MAR-1993
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Moran, Thomas F
;      REGISTRATION NUMBER:  16,579
;      REFERENCE/DOCKET NUMBER:  43276
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212)-977-9550
;      TELEFAX:  (212)-977-9809
;      TELEX:  422523 COOP UI
;  INFORMATION FOR SEQ ID NO:  10:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  12 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-030-335-10

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 12;
  Best Local Similarity   90.0%;  Pred. No. 9.2;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          7 GGTCACATGG 16
              ||||||  |||
Db         12 GGTCACGTGG 3


RESULT 9
US-07-973-431B-3/c
; Sequence 3, Application US/07973431B
; Patent No. 5652144
;  GENERAL INFORMATION:
;    APPLICANT:  Lu, Yinchen
;    APPLICANT:  Haseltine, William A
;    TITLE OF INVENTION:  YC1 Protein, Gene, And Uses Thereof
;    NUMBER OF SEQUENCES:  5
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  David G. Conlin; Dike, Bronstein,
;      ADDRESSEE:  Roberts & Cushman
;      STREET:  130 Water Street
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/973,431B
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Eisenstein, Ronald I
;      REGISTRATION NUMBER:  30628
;      REFERENCE/DOCKET NUMBER:  41968
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617) 523-3400
;      TELEFAX:  (617) 523-6440
;      TELEX:  200291 STRE UR
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  12 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  unknown
;      TOPOLOGY:  unknown
US-07-973-431B-3

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 12;
  Best Local Similarity   90.0%;  Pred. No. 9.2;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          7 GGTCACATGG 16
              ||||||  |||
Db         12 GGTCACGTGG 3


RESULT 10
US-08-122-433-26/c
; Sequence 26, Application US/08122433
; Patent No. 5683985
;  GENERAL INFORMATION:
;    APPLICANT:  Chu, Barbara C.F.
;    APPLICANT:  Orgel, Leslie
;    TITLE OF INVENTION:  OLIGODEOXYNUCLEOTIDES AND
;    TITLE OF INVENTION:  OLIGONUCLEOTIDES USEFUL AS DECOYS FOR PROTEINS WHICH
;    TITLE OF INVENTION:  SELECTIVELY BIND TO DEFINED DNA SEQUENCES
;    NUMBER OF SEQUENCES:  47
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  PRETTY, SCHROEDER, BRUEGGEMANN & CLARK
;      STREET:  444 South Flower Street, Suite 2000
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  90071
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/122,433
;      FILING DATE:  22-SEP-1993
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/687,337
;      FILING DATE:  18-APR-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Reiter, Stephen E.
;      REGISTRATION NUMBER:  31,192
;      REFERENCE/DOCKET NUMBER:  P31 9308
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  619-546-1995
;      TELEFAX:  619-546-9392
;  INFORMATION FOR SEQ ID NO:  26:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  12 base pairs
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;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  other nucleic acid
US-08-122-433-26

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 12;
  Best Local Similarity   90.0%;  Pred. No. 9.2;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          7 GGTCACATGG 16
              |||||| |||
Db         12 GGTCACGTGG 3


RESULT 11
US-08-623-891-24/c
; Sequence 24, Application US/08623891
; Patent No. 5795778
;  GENERAL INFORMATION:
;    APPLICANT:  Kenneth G. Draper
;    TITLE OF INVENTION:  METHOD AND REAGENT FOR
;    TITLE OF INVENTION:  INHIBITING HERPES SIMPLEX
;    TITLE OF INVENTION:  VIRUS REPLICATION
;    NUMBER OF SEQUENCES:  115
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lyon & Lyon
;      STREET:  611 West Sixth Street
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  90017
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb storage
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  IBM P.C. DOS (Version 5.0)
;      SOFTWARE:  WordPerfect (Version 5.1)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/623,891
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/238,200
;      FILING DATE:
;      APPLICATION NUMBER:  US/07/987,133
;      FILING DATE:
;      APPLICATION NUMBER:  07/882,921
;      FILING DATE:  May 14, 1992
;      APPLICATION NUMBER:  07/948,359
;      FILING DATE:  September 18, 1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Warburg, Richard J.
;      REGISTRATION NUMBER:  32,327
;      REFERENCE/DOCKET NUMBER:  200/209
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (213) 489-1600
;      TELEFAX:  (213) 955-0440
;      TELEX:  67-3510
;  INFORMATION FOR SEQ ID NO:  24:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  12
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-623-891-24

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 12;
  Best Local Similarity   90.0%;  Pred. No. 9.2;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 TCATGGTCAC 12
              |||||| |||
Db         12 TCATGGCCAC 3


RESULT 12
US-08-480-020B-10/c
; Sequence 10, Application US/08480020B
; Patent No. 5932476
;  GENERAL INFORMATION:
;    APPLICANT:  NOTEBORN, MATHEUS H.M.
;    APPLICANT:  DE BOER, GERDEN F.
;    TITLE OF INVENTION:  CLONING OF CHICKEN ANEMIA DNA
;    NUMBER OF SEQUENCES:  38
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  RAE-VENTER LAW GROUP
;      STREET:  260 SHERIDAN AVENUE, SUITE 400
;      CITY:  PALO ALTO
;      STATE:  CALIFORNIA
;      COUNTRY:  UNITED STATES OF AMERICA
;      ZIP:  94306
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/480,020B
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/030,335
;      FILING DATE:  08-MAR-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  WO PCT/NL91/00165
;      FILING DATE:  12-SEP-1990
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  NL 9002008
;      FILING DATE:  12-SEP-1990
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  KUNG, VIOLA
;      REGISTRATION NUMBER:  P41,131
;      REFERENCE/DOCKET NUMBER:  VEOC.002.02US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (650)328-4400
;      TELEFAX:  (650)328-4477
;  INFORMATION FOR SEQ ID NO:  10:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  12 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-480-020B-10

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 12;
  Best Local Similarity   90.0%;  Pred. No. 9.2;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          7 GGTCACATGG 16
              |||||| |||
Db         12 GGTCACGTGG 3


RESULT 13
US-08-910-618-10/c
; Sequence 10, Application US/08910618
; Patent No. 5958424
;  GENERAL INFORMATION:
;    APPLICANT:  NOTEBORN, MATHEUS H.M.
;    APPLICANT:  DE BOER, GERDEN F.
;    TITLE OF INVENTION:  CLONING OF CHICKEN ANEMIA DNA
;    NUMBER OF SEQUENCES:  28
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  RAE-VENTER LAW GROUP
;      STREET:  260 SHERIDAN AVENUE, SUITE 400
```

```
;      CITY:  PALO ALTO
;      STATE:  CALIFORNIA
;      COUNTRY:  UNITED STATES OF AMERICA
;      ZIP:  94306
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/910,618
;      FILING DATE:  13-AUG-1997
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/484,939
;      FILING DATE:  07-JUN-1995
;      APPLICATION NUMBER:  US 08/030,335
;      FILING DATE:  08-MAR-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  WO PCT/NL91/00165
;      FILING DATE:  12-SEP-1990
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  NL 9002008
;      FILING DATE:  12-SEP-1990
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Rae-Venter, Barbara
;      REGISTRATION NUMBER:  32,750
;      REFERENCE/DOCKET NUMBER:  VEOC.002.01US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (650)328-4400
;      TELEFAX:  (650)328-4477
;  INFORMATION FOR SEQ ID NO:  10:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  12 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-910-618-10

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 12;
  Best Local Similarity   90.0%;  Pred. No. 9.2;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          7 GGTCACATGG 16
              |||||| |||
Db         12 GGTCACGTGG 3


RESULT 14
US-09-105-515-2/c
; Sequence 2, Application US/09105515
; Patent No. 6113913
;  GENERAL INFORMATION:
;    APPLICANT:  BROUGH, DOUGLAS E.
;    TITLE OF INVENTION:  RECOMBINANT ADENOVIRUS
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  LEYDIG, VOIT & MAYER, LTD.
;      STREET:  TWO PRUDENTIAL PLAZA, SUITE 4900
;      CITY:  CHICAGO
;      STATE:  IL
;      COUNTRY:  US
;      ZIP:  60601-6780
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/105,515
;      FILING DATE:
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  KILYK JR., JOHN
;      REGISTRATION NUMBER:  30763
;      REFERENCE/DOCKET NUMBER:  83827
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  312-616-5600
;      TELEFAX:  312-616-5700
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  12 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  unknown
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  DNA (genomic)
US-09-105-515-2

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 12;
  Best Local Similarity   90.0%;  Pred. No. 9.2;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          7 GGTCACATGG 16
              |||||| |||
Db         12 GGTCACGTGG 3


RESULT 15
US-08-910-322-10/c
; Sequence 10, Application US/08910322
; Patent No. 6238669
;  GENERAL INFORMATION:
;    APPLICANT:  NOTEBORN, MATHEUS H.M.
;    APPLICANT:  DE BOER, GERDEN F.
;    TITLE OF INVENTION:  CLONING OF CHICKEN ANEMIA DNA
;    NUMBER OF SEQUENCES:  28
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  RAE-VENTER LAW GROUP
;      STREET:  260 SHERIDAN AVENUE, SUITE 400
;      CITY:  PALO ALTO
;      STATE:  CALIFORNIA
;      COUNTRY:  UNITED STATES OF AMERICA
;      ZIP:  94306
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/910,322
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/484,939
;      FILING DATE:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  WO PCT/NL91/00165
;      FILING DATE:  12-SEP-1990
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  NL 9002008
;      FILING DATE:  12-SEP-1990
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Rae-Venter, Barbara
;      REGISTRATION NUMBER:  32,750
;      REFERENCE/DOCKET NUMBER:  VEOC.002.01US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (650)328-4400
;      TELEFAX:  (650)328-4477
;  INFORMATION FOR SEQ ID NO:  10:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  12 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
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```
US-08-910-322-10

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 12;
  Best Local Similarity   90.0%;  Pred. No. 9.2;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          7 GGTCACATGG 16
              |||||| |||
Db         12 GGTCACGTGG 3


RESULT 16
US-08-679-493A-68/c
; Sequence 68, Application US/08679493A
; Patent No. 6303295
; GENERAL INFORMATION:
;  APPLICANT: Taylor, Ethan W.
;  TITLE OF INVENTION: SELENOPROTEINS, CODING SEQUENCES AND METHODS
;  FILE REFERENCE: 55-95
;  CURRENT APPLICATION NUMBER: US/08/679,493A
;  CURRENT FILING DATE:  1996-07-12
;  PRIOR APPLICATION NUMBER: 60/001203
;  PRIOR FILING DATE: 1995-07-14
;  PRIOR APPLICATION NUMBER: 60/003,112
;  PRIOR FILING DATE: 1995-09-01
;  NUMBER OF SEQ ID NOS: 216
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 68
;   LENGTH: 12
;   TYPE: RNA
;   ORGANISM: Human immunodeficiency virus type 1
US-08-679-493A-68

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 12;
  Best Local Similarity   90.0%;  Pred. No. 9.2;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 CTCATGGTCA 11
              |||| |||||
Db         11 CTCAGGGTCA 2


RESULT 17
US-08-484-939A-10/c
; Sequence 10, Application US/08484939A
; Patent No. 6319693
;  GENERAL INFORMATION:
;    APPLICANT:  NOTEBORN, MATHEUS H.M.
;    APPLICANT:  DE BOER, GERDEN F.
;    TITLE OF INVENTION:  CLONING OF CHICKEN ANEMIA DNA
;    NUMBER OF SEQUENCES:  28
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  RAE-VENTER LAW GROUP
;      STREET:  260 SHERIDAN AVENUE, SUITE 400
;      CITY:  PALO ALTO
;      STATE:  CALIFORNIA
;      COUNTRY:  UNITED STATES OF AMERICA
;      ZIP:  94306
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/484,939A
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/030,335
;      FILING DATE:  08-MAR-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  WO PCT/NL91/00165
;      FILING DATE:  12-SEP-1990
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  NL 9002008
;      FILING DATE:  12-SEP-1990
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Rae-Venter, Barbara
;      REGISTRATION NUMBER:  32,750
;      REFERENCE/DOCKET NUMBER:  VEOC.002.01US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (650)328-4400
;      TELEFAX:  (650)328-4477
;  INFORMATION FOR SEQ ID NO:  10:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  12 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-484-939A-10

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 12;
  Best Local Similarity   90.0%;  Pred. No. 9.2;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          7 GGTCACATGG 16
              |||||| |||
Db         12 GGTCACGTGG 3


RESULT 18
US-09-340-861-24/c
; Sequence 24, Application US/09340861
; Patent No. 6432704
;  GENERAL INFORMATION:
;    APPLICANT:  Kenneth G. Draper
;    TITLE OF INVENTION:  METHOD AND REAGENT FOR
;    TITLE OF INVENTION:  INHIBITING HERPES SIMPLEX
;    TITLE OF INVENTION:  VIRUS REPLICATION
;    NUMBER OF SEQUENCES:  115
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lyon & Lyon
;      STREET:  611 West Sixth Street
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  90017
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb storage
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  IBM P.C. DOS (Version 5.0)
;      SOFTWARE:  WordPerfect (Version 5.1)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/340,861
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/987,133
;      FILING DATE:
;      APPLICATION NUMBER:  07/882,921
;      FILING DATE:  May 14, 1992
;      APPLICATION NUMBER:  07/948,359
;      FILING DATE:  September 18, 1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Warburg, Richard J.
;      REGISTRATION NUMBER:  32,327
;      REFERENCE/DOCKET NUMBER:  200/209
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (213) 489-1600
;      TELEFAX:  (213) 955-0440
;      TELEX:  67-3510
;  INFORMATION FOR SEQ ID NO:  24:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  12
;      TYPE:  nucleic acid
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;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-09-340-861-24

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 12;
  Best Local Similarity   90.0%;  Pred. No. 9.2;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 TCATGGTCAC 12
              |||||| |||
Db         12 TCATGGCCAC 3


RESULT 19
US-09-634-262-24/c
; Sequence 24, Application US/09634262
; Patent No. 6440719
;  GENERAL INFORMATION:
;    APPLICANT:  Kenneth G. Draper
;    TITLE OF INVENTION:  METHOD AND REAGENT FOR
;    TITLE OF INVENTION:  INHIBITING HERPES SIMPLEX
;    TITLE OF INVENTION:  VIRUS REPLICATION
;    NUMBER OF SEQUENCES:  115
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lyon & Lyon
;      STREET:  611 West Sixth Street
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  90017
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb storage
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  IBM P.C. DOS (Version 5.0)
;      SOFTWARE:  WordPerfect (Version 5.1)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/634,262
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/987,133
;      FILING DATE:
;      APPLICATION NUMBER:  07/882,921
;      FILING DATE:  May 14, 1992
;      APPLICATION NUMBER:  07/948,359
;      FILING DATE:  September 18, 1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Warburg, Richard J.
;      REGISTRATION NUMBER:  32,327
;      REFERENCE/DOCKET NUMBER:  200/209
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (213) 489-1600
;      TELEFAX:  (213) 955-0440
;      TELEX:  67-3510
;  INFORMATION FOR SEQ ID NO:  24:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  12
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-09-634-262-24

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 12;
  Best Local Similarity   90.0%;  Pred. No. 9.2;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 TCATGGTCAC 12
              |||||| |||
Db         12 TCATGGCCAC 3


RESULT 20
US-09-748-044-2/c
; Sequence 2, Application US/09748044
; Patent No. 6458578
; GENERAL INFORMATION:
;  APPLICANT: Brough, Douglas E.
;  APPLICANT:  Kovesdi, Imre
;  TITLE OF INVENTION: Recombinant Cell Line
;  FILE REFERENCE: 207952
;  CURRENT APPLICATION NUMBER: US/09/748,044
;  CURRENT FILING DATE:  2000-12-22
;  PRIOR APPLICATION NUMBER: PCT/US99/14333
;  PRIOR FILING DATE: 1999-06-24
;  PRIOR APPLICATION NUMBER: US 09/105,515
;  PRIOR FILING DATE: 1998-06-26
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
;   LENGTH: 12
;   TYPE: DNA
;   ORGANISM: Adenovirus type 5
US-09-748-044-2

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 12;
  Best Local Similarity   90.0%;  Pred. No. 9.2;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          7 GGTCACATGG 16
              |||||| |||
Db         12 GGTCACGTGG 3


RESULT 21
US-09-384-472-10/c
; Sequence 10, Application US/09384472
; Patent No. 6509446
;  GENERAL INFORMATION:
;    APPLICANT:  NOTEBORN, MATHEUS H.M.
;    APPLICANT:  DE BOER, GERDEN F.
;    TITLE OF INVENTION:  CLONING OF CHICKEN ANEMIA DNA
;    NUMBER OF SEQUENCES:  28
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  RAE-VENTER LAW GROUP
;      STREET:  260 SHERIDAN AVENUE, SUITE 400
;      CITY:  PALO ALTO
;      STATE:  CALIFORNIA
;      COUNTRY:  UNITED STATES OF AMERICA
;      ZIP:  94306
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/384,472
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/484,939
;      FILING DATE:  07-JUN-1995
;      APPLICATION NUMBER:  US 08/030,335
;      FILING DATE:  08-MAR-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  WO PCT/NL91/00165
;      FILING DATE:  12-SEP-1990
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  NL 9002008
;      FILING DATE:  12-SEP-1990
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Rae-Venter, Barbara
;      REGISTRATION NUMBER:  32,750
;      REFERENCE/DOCKET NUMBER:  VEOC.002.01US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (650)328-4400
;      TELEFAX:  (650)328-4477
```

```
;  INFORMATION FOR SEQ ID NO:  10:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  12 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-09-384-472-10

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 12;
  Best Local Similarity   90.0%;  Pred. No. 9.2;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          7 GGTCACATGG 16
              |||||| |||
Db         12 GGTCACGTGG 3


RESULT 22
US-09-835-370-54
; Sequence 54, Application US/09835370
; Patent No. 6777544
; GENERAL INFORMATION:
;  APPLICANT: UHLMANN, EUGEN
;  APPLICANT:  BREIPOHL, GERHARD
;  APPLICANT:  WILL, DAVID W
;  TITLE OF INVENTION: POLYAMIDE NUCLEIC ACID DERIVATIVES AND AGENTS AND
;  TITLE OF INVENTION:  PROCESSES FOR PREPARING THEM
;  FILE REFERENCE: 02481.1742 SEQUENCE LISTING
;  CURRENT APPLICATION NUMBER: US/09/835,370
;  CURRENT FILING DATE:  2001-04-17
;  NUMBER OF SEQ ID NOS: 64
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 54
;   LENGTH: 12
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  nucleotide
;   OTHER INFORMATION: base sequence of PNA derivatives that bind to
;   OTHER INFORMATION: viral and cellular targets
US-09-835-370-54

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 12;
  Best Local Similarity   90.0%;  Pred. No. 9.2;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 CCTCATGGTC 10
              | ||||||||
Db          2 CATCATGGTC 11


RESULT 23
US-09-793-146-38
; Sequence 38, Application US/09793146
; Patent No. 6919441
; GENERAL INFORMATION:
;  APPLICANT: UHLMANN, EUGEN
;  APPLICANT:  BREIPOHL, GERHARD
;  TITLE OF INVENTION: POLYAMIDE-OLIGONUCLEOTIDE DERIVATIVES, THEIR
;  TITLE OF INVENTION:  PREPARATION AND USE
;  FILE REFERENCE: 02481.1437-02
;  CURRENT APPLICATION NUMBER: US/09/793,146
;  CURRENT FILING DATE:  2001-02-27
;  PRIOR APPLICATION NUMBER: P 44 08 528.1
;  PRIOR FILING DATE: 1994-03-14
;  PRIOR APPLICATION NUMBER: 08/402,838
;  PRIOR FILING DATE: 1995-03-13
;  NUMBER OF SEQ ID NOS: 70
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 38
;   LENGTH: 12
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic PNA
US-09-793-146-38

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 12;
  Best Local Similarity   90.0%;  Pred. No. 9.2;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 CCTCATGGTC 10
              | ||||||||
Db          2 CATCATGGTC 11


RESULT 24
US-09-793-146-48
; Sequence 48, Application US/09793146
; Patent No. 6919441
; GENERAL INFORMATION:
;  APPLICANT: UHLMANN, EUGEN
;  APPLICANT:  BREIPOHL, GERHARD
;  TITLE OF INVENTION: POLYAMIDE-OLIGONUCLEOTIDE DERIVATIVES, THEIR
;  TITLE OF INVENTION:  PREPARATION AND USE
;  FILE REFERENCE: 02481.1437-02
;  CURRENT APPLICATION NUMBER: US/09/793,146
;  CURRENT FILING DATE:  2001-02-27
;  PRIOR APPLICATION NUMBER: P 44 08 528.1
;  PRIOR FILING DATE: 1994-03-14
;  PRIOR APPLICATION NUMBER: 08/402,838
;  PRIOR FILING DATE: 1995-03-13
;  NUMBER OF SEQ ID NOS: 70
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 48
;   LENGTH: 12
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic PNA
US-09-793-146-48

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 12;
  Best Local Similarity   90.0%;  Pred. No. 9.2;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 CCTCATGGTC 10
              | ||||||||
Db          2 CATCATGGTC 11


RESULT 25
US-09-793-146-49/c
; Sequence 49, Application US/09793146
; Patent No. 6919441
; GENERAL INFORMATION:
;  APPLICANT: UHLMANN, EUGEN
;  APPLICANT:  BREIPOHL, GERHARD
;  TITLE OF INVENTION: POLYAMIDE-OLIGONUCLEOTIDE DERIVATIVES, THEIR
;  TITLE OF INVENTION:  PREPARATION AND USE
;  FILE REFERENCE: 02481.1437-02
;  CURRENT APPLICATION NUMBER: US/09/793,146
;  CURRENT FILING DATE:  2001-02-27
;  PRIOR APPLICATION NUMBER: P 44 08 528.1
;  PRIOR FILING DATE: 1994-03-14
;  PRIOR APPLICATION NUMBER: 08/402,838
;  PRIOR FILING DATE: 1995-03-13
;  NUMBER OF SEQ ID NOS: 70
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 49
;   LENGTH: 12
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic PNA
```

US-09-793-146-49

Query Match 42.0%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 9.2;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy          1 CCTCATGGTC 10
              | ||||||||
Db         11 CATCATGGTC 2
```

Search completed: June 13, 2006, 15:51:50
Job time : 0.001 secs

GenCore version 5.1.9

OM nucleic - nucleic search, using sw model

Run on: June 13, 2006, 15:50:13 ; Search time 0.001 Seconds
(without alignments)
27.080 Million cell updates/sec

Title: US-10-719-370A-446
Perfect score: 20
Sequence: 1 cctcatggtcacatggatga 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 0.5

Searched: 37 seqs, 677 residues

Total number of hits satisfying chosen parameters: 74

Minimum DB seq length: 12
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 37 summaries

Database : us-10-719-370a-446.sl.rnpbm4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	20	100.0	20	1	US-10-719-370A-446	Sequence 446, App
	2	19	95.0	20	1	US-10-719-370A-141	Sequence 141, App
	3	19	95.0	20	1	US-10-719-370A-447	Sequence 447, App
	4	18	90.0	20	1	US-10-719-370A-445	Sequence 445, App
	5	18	90.0	20	1	US-10-719-370A-452	Sequence 452, App
	6	17	85.0	20	1	US-10-766-185-26	Sequence 26, Appl
	7	17	85.0	20	1	US-10-719-370A-451	Sequence 451, App
	8	16.8	84.0	20	1	US-10-719-370A-443	Sequence 443, App
	9	16	80.0	20	1	US-10-719-370A-448	Sequence 448, App
	10	15.8	79.0	20	1	US-10-719-370A-450	Sequence 450, App
c	11	14.4	72.0	19	1	US-10-310-914A-757115	Sequence 757115,
	12	14.4	72.0	19	1	US-11-083-784-440242	Sequence 440242,
	13	14.4	72.0	19	1	US-11-101-244-440242	Sequence 440242,
c	14	13.8	69.0	19	1	US-11-083-784-15285	Sequence 15285, A
	15	13.8	69.0	19	1	US-11-083-784-144519	Sequence 144519,
	16	13.8	69.0	19	1	US-11-083-784-1218947	Sequence 1218947,
c	17	13.8	69.0	19	1	US-11-101-244-15285	Sequence 15285, A
	18	13.8	69.0	19	1	US-11-101-244-144519	Sequence 144519,
	19	13.8	69.0	19	1	US-11-101-244-1218947	Sequence 1218947,
c	20	13.4	67.0	19	1	US-11-083-784-155627	Sequence 155627,
c	21	13.4	67.0	19	1	US-11-083-784-155645	Sequence 155645,
	22	13.4	67.0	19	1	US-11-083-784-943972	Sequence 943972,
c	23	13.4	67.0	19	1	US-11-083-784-1009396	Sequence 1009396,
	24	13.4	67.0	19	1	US-11-083-784-1224506	Sequence 1224506,
c	25	13.4	67.0	19	1	US-11-101-244-155627	Sequence 155627,
c	26	13.4	67.0	19	1	US-11-101-244-155645	Sequence 155645,
	27	13.4	67.0	19	1	US-11-101-244-943972	Sequence 943972,
c	28	13.4	67.0	19	1	US-11-101-244-1009396	Sequence 1009396,
	29	13.4	67.0	19	1	US-11-101-244-1224506	Sequence 1224506,
c	30	12.2	61.0	17	1	US-09-866-108-7612	Sequence 7612, Ap
c	31	12.2	61.0	17	1	US-10-723-361-7612	Sequence 7612, Ap
	32	11.4	57.0	15	1	US-09-916-466-30	Sequence 30, Appl
	33	11.4	57.0	15	1	US-10-277-494-30	Sequence 30, Appl
	34	9.8	49.0	13	1	US-10-257-017B-228161	Sequence 228161,
c	35	9.8	49.0	13	1	US-10-257-017B-228162	Sequence 228162,
	36	9.8	49.0	13	1	US-10-257-017B-245261	Sequence 245261,
c	37	9.8	49.0	13	1	US-10-257-017B-245262	Sequence 245262,

ALIGNMENTS

RESULT 1
US-10-719-370A-446
; Sequence 446, Application US/10719370A
; Publication No. US20040220393A1
; GENERAL INFORMATION:
; APPLICANT: Ward, Donna T.
; APPLICANT: Dobie, Kenneth W.
; APPLICANT: Marcusson, Eric G.
; APPLICANT: Freier, Susan M.
; TITLE OF INVENTION: MODULATION OF HIF1a AND HIF2a EXPRESSION
; FILE REFERENCE: ISPT-1010
; CURRENT APPLICATION NUMBER: US/10/719,370A
; CURRENT FILING DATE: 2003-11-21
; PRIOR APPLICATION NUMBER: US 10/304,126
; PRIOR FILING DATE: 2002-11-23
; NUMBER OF SEQ ID NOS: 458
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 446
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-719-370A-446

Query Match 100.0%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTCATGGTCACATGGATGA 20
||||||||||||||||||||
Db 1 CCTCATGGTCACATGGATGA 20

RESULT 2
US-10-719-370A-141
; Sequence 141, Application US/10719370A
; Publication No. US20040220393A1
; GENERAL INFORMATION:
; APPLICANT: Ward, Donna T.
; APPLICANT: Dobie, Kenneth W.
; APPLICANT: Marcusson, Eric G.
; APPLICANT: Freier, Susan M.
; TITLE OF INVENTION: MODULATION OF HIF1a AND HIF2a EXPRESSION
; FILE REFERENCE: ISPT-1010
; CURRENT APPLICATION NUMBER: US/10/719,370A
; CURRENT FILING DATE: 2003-11-21
; PRIOR APPLICATION NUMBER: US 10/304,126
; PRIOR FILING DATE: 2002-11-23
; NUMBER OF SEQ ID NOS: 458
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 141
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-719-370A-141

Query Match 95.0%; Score 19; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.4;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTCATGGTCACATGGATG 19

```
                    ||||||||||||||||||
Db          2 CCTCATGGTCACATGGATG 20


RESULT 3
US-10-719-370A-447
; Sequence 447, Application US/10719370A
; Publication No. US20040220393A1
; GENERAL INFORMATION:
;  APPLICANT: Ward, Donna T.
;  APPLICANT:  Dobie, Kenneth W.
;  APPLICANT:  Marcusson, Eric G.
;  APPLICANT:  Freier, Susan M.
;  TITLE OF INVENTION: MODULATION OF HIF1a AND HIF2a EXPRESSION
;  FILE REFERENCE: ISPT-1010
;  CURRENT APPLICATION NUMBER: US/10/719,370A
;  CURRENT FILING DATE:  2003-11-21
;  PRIOR APPLICATION NUMBER: US 10/304,126
;  PRIOR FILING DATE: 2002-11-23
;  NUMBER OF SEQ ID NOS: 458
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 447
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic Construct
US-10-719-370A-447

  Query Match             95.0%;  Score 19;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 3.4;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 CTCATGGTCACATGGATGA 20
              ||||||||||||||||||||
Db          1 CTCATGGTCACATGGATGA 19


RESULT 4
US-10-719-370A-445
; Sequence 445, Application US/10719370A
; Publication No. US20040220393A1
; GENERAL INFORMATION:
;  APPLICANT: Ward, Donna T.
;  APPLICANT:  Dobie, Kenneth W.
;  APPLICANT:  Marcusson, Eric G.
;  APPLICANT:  Freier, Susan M.
;  TITLE OF INVENTION: MODULATION OF HIF1a AND HIF2a EXPRESSION
;  FILE REFERENCE: ISPT-1010
;  CURRENT APPLICATION NUMBER: US/10/719,370A
;  CURRENT FILING DATE:  2003-11-21
;  PRIOR APPLICATION NUMBER: US 10/304,126
;  PRIOR FILING DATE: 2002-11-23
;  NUMBER OF SEQ ID NOS: 458
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 445
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic Construct
US-10-719-370A-445

  Query Match             90.0%;  Score 18;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.5;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 TCATGGTCACATGGATGA 20
              ||||||||||||||||||
Db          1 TCATGGTCACATGGATGA 18


RESULT 5
```

```
US-10-719-370A-452
; Sequence 452, Application US/10719370A
; Publication No. US20040220393A1
; GENERAL INFORMATION:
;  APPLICANT: Ward, Donna T.
;  APPLICANT:  Dobie, Kenneth W.
;  APPLICANT:  Marcusson, Eric G.
;  APPLICANT:  Freier, Susan M.
;  TITLE OF INVENTION: MODULATION OF HIF1a AND HIF2a EXPRESSION
;  FILE REFERENCE: ISPT-1010
;  CURRENT APPLICATION NUMBER: US/10/719,370A
;  CURRENT FILING DATE:  2003-11-21
;  PRIOR APPLICATION NUMBER: US 10/304,126
;  PRIOR FILING DATE: 2002-11-23
;  NUMBER OF SEQ ID NOS: 458
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 452
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic Construct
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (11)..(11)
;   OTHER INFORMATION: n = inosine
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (14)..(14)
;   OTHER INFORMATION: n = pseudouridine
US-10-719-370A-452

  Query Match             90.0%;  Score 18;  DB 1;  Length 20;
  Best Local Similarity   90.0%;  Pred. No. 4.5;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 CCTCATGGTCACATGGATGA 20
              |||||||||| || ||||||
Db          1 CCTCATGGTCNCANGGATGA 20


RESULT 6
US-10-766-185-26
; Sequence 26, Application US/10766185
; Publication No. US20040152655A1
; GENERAL INFORMATION:
;  APPLICANT: Yoon, Heejeong
;  APPLICANT:  Ahn, Chang Ho
;  APPLICANT:  Lee, Young  Bok
;  APPLICANT:  Mao, Lingjun
;  APPLICANT:  Jiang, Xiaoming
;  TITLE OF INVENTION: Antisense Oligonucleotides that inhibit expression of HIF-1
;  FILE REFERENCE: REX 7034
;  CURRENT APPLICATION NUMBER: US/10/766,185
;  CURRENT FILING DATE:  2004-01-28
;  NUMBER OF SEQ ID NOS: 130
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 26
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: artificial sequence
;   FEATURE:
;   OTHER INFORMATION: antisense oligonucleotide
US-10-766-185-26

  Query Match             85.0%;  Score 17;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 5.8;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 CATGGTCACATGGATGA 20
              |||||||||||||||||
Db          1 CATGGTCACATGGATGA 17
```

```
RESULT 7
US-10-719-370A-451
; Sequence 451, Application US/10719370A
; Publication No. US20040220393A1
; GENERAL INFORMATION:
;  APPLICANT: Ward, Donna T.
;  APPLICANT:  Dobie, Kenneth W.
;  APPLICANT:  Marcusson, Eric G.
;  APPLICANT:  Freier, Susan M.
;  TITLE OF INVENTION: MODULATION OF HIF1a AND HIF2a EXPRESSION
;  FILE REFERENCE: ISPT-1010
;  CURRENT APPLICATION NUMBER: US/10/719,370A
;  CURRENT FILING DATE:  2003-11-21
;  PRIOR APPLICATION NUMBER: US 10/304,126
;  PRIOR FILING DATE: 2002-11-23
;  NUMBER OF SEQ ID NOS: 458
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 451
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic Construct
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (12)..(12)
;   OTHER INFORMATION: n = inosine
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (15)..(15)
;   OTHER INFORMATION: n = pseudouridine
US-10-719-370A-451

  Query Match             85.0%;  Score 17;  DB 1;  Length 20;
  Best Local Similarity   89.5%;  Pred. No. 5.8;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 CCTCATGGTCACATGGATG 19
              ||||||||||  || |||||
Db          2 CCTCATGGTCNCANGGATG 20


RESULT 8
US-10-719-370A-443
; Sequence 443, Application US/10719370A
; Publication No. US20040220393A1
; GENERAL INFORMATION:
;  APPLICANT: Ward, Donna T.
;  APPLICANT:  Dobie, Kenneth W.
;  APPLICANT:  Marcusson, Eric G.
;  APPLICANT:  Freier, Susan M.
;  TITLE OF INVENTION: MODULATION OF HIF1a AND HIF2a EXPRESSION
;  FILE REFERENCE: ISPT-1010
;  CURRENT APPLICATION NUMBER: US/10/719,370A
;  CURRENT FILING DATE:  2003-11-21
;  PRIOR APPLICATION NUMBER: US 10/304,126
;  PRIOR FILING DATE: 2002-11-23
;  NUMBER OF SEQ ID NOS: 458
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 443
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic Construct
US-10-719-370A-443

  Query Match             84.0%;  Score 16.8;  DB 1;  Length 20;
  Best Local Similarity   90.0%;  Pred. No. 6.1;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 CCTCATGGTCACATGGATGA 20
              ||||||||||  || ||||||
Db          1 CCTCATGGTCGCAGGGATGA 20


RESULT 9
US-10-719-370A-448
; Sequence 448, Application US/10719370A
; Publication No. US20040220393A1
; GENERAL INFORMATION:
;  APPLICANT: Ward, Donna T.
;  APPLICANT:  Dobie, Kenneth W.
;  APPLICANT:  Marcusson, Eric G.
;  APPLICANT:  Freier, Susan M.
;  TITLE OF INVENTION: MODULATION OF HIF1a AND HIF2a EXPRESSION
;  FILE REFERENCE: ISPT-1010
;  CURRENT APPLICATION NUMBER: US/10/719,370A
;  CURRENT FILING DATE:  2003-11-21
;  PRIOR APPLICATION NUMBER: US 10/304,126
;  PRIOR FILING DATE: 2002-11-23
;  NUMBER OF SEQ ID NOS: 458
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 448
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic Construct
US-10-719-370A-448

  Query Match             80.0%;  Score 16;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 7.5;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CCTCATGGTCACATGG 16
              ||||||||||||||||
Db          5 CCTCATGGTCACATGG 20


RESULT 10
US-10-719-370A-450
; Sequence 450, Application US/10719370A
; Publication No. US20040220393A1
; GENERAL INFORMATION:
;  APPLICANT: Ward, Donna T.
;  APPLICANT:  Dobie, Kenneth W.
;  APPLICANT:  Marcusson, Eric G.
;  APPLICANT:  Freier, Susan M.
;  TITLE OF INVENTION: MODULATION OF HIF1a AND HIF2a EXPRESSION
;  FILE REFERENCE: ISPT-1010
;  CURRENT APPLICATION NUMBER: US/10/719,370A
;  CURRENT FILING DATE:  2003-11-21
;  PRIOR APPLICATION NUMBER: US 10/304,126
;  PRIOR FILING DATE: 2002-11-23
;  NUMBER OF SEQ ID NOS: 458
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 450
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic Construct
US-10-719-370A-450

  Query Match             79.0%;  Score 15.8;  DB 1;  Length 20;
  Best Local Similarity   89.5%;  Pred. No. 7.9;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 CCTCATGGTCACATGGATG 19
              ||||||||||  || |||||
Db          2 CCTCATGGTCGCAGGGATG 20


RESULT 11
```

```
US-10-310-914A-757115/c
; Sequence 757115, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
;  APPLICANT: Bentwich, Isaac
;  APPLICANT:  Shiler, Kvuzat
;  TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
;  TITLE OF INVENTION:  uses thereof
;  FILE REFERENCE: 06087.0200.CPUS01
;  CURRENT APPLICATION NUMBER: US/10/310,914A
;  CURRENT FILING DATE:  2002-12-06
;  NUMBER OF SEQ ID NOS: 1388402
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 757115
;   LENGTH: 19
;   TYPE: RNA
;   ORGANISM: Human
US-10-310-914A-757115

  Query Match             72.0%;  Score 14.4;  DB 1;  Length 19;
  Best Local Similarity   93.8%;  Pred. No. 10;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 CCTCATGGTCACATGG 16
              ||| ||||||||||||
Db         18 CCTGATGGTCACATGG 3


RESULT 12
US-11-083-784-440242
; Sequence 440242, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
;  APPLICANT: Dharmacon, Inc.
;  APPLICANT:  Khvorova, Anastasia
;  APPLICANT:  Reynolds, Angela
;  APPLICANT:  Leake, Devin
;  APPLICANT:  Marshall, William
;  APPLICANT:  Scaringe, Stephen
;  TITLE OF INVENTION: Functional and Hyperfunctional siRNA
;  FILE REFERENCE: 13499US
;  CURRENT APPLICATION NUMBER: US/11/083,784
;  CURRENT FILING DATE:  2005-03-18
;  PRIOR APPLICATION NUMBER: US/10/714,333
;  PRIOR FILING DATE: 2003-11-14
;  PRIOR APPLICATION NUMBER: 60/502,050
;  PRIOR FILING DATE: 2003-09-10
;  PRIOR APPLICATION NUMBER: 60/426,137
;  PRIOR FILING DATE: 2002-11-14
;  NUMBER OF SEQ ID NOS: 1591911
;  SOFTWARE: Proprietary
; SEQ ID NO 440242
;   LENGTH: 19
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-11-083-784-440242

  Query Match             72.0%;  Score 14.4;  DB 1;  Length 19;
  Best Local Similarity   75.0%;  Pred. No. 10;
  Matches   12;  Conservative    3;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          5 ATGGTCACATGGATGA 20
              | ||:||||:|||:||
Db          4 AAGGUCACAUGGAUGA 19


RESULT 13
US-11-101-244-440242
; Sequence 440242, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
;  APPLICANT: Dharmacon, Inc.
;  APPLICANT:  Khvorova, Anastasia
;  APPLICANT:  Reynolds, Angela
;  APPLICANT:  Leake, Devin
;  APPLICANT:  Marshall, William
;  APPLICANT:  Scaringe, Stephen
;  TITLE OF INVENTION: Functional and Hyperfunctional siRNA
;  FILE REFERENCE: 13499US
;  CURRENT APPLICATION NUMBER: US/11/101,244
;  CURRENT FILING DATE:  2005-04-07
;  PRIOR APPLICATION NUMBER: 60/502,050
;  PRIOR FILING DATE: 2003-09-10
;  PRIOR APPLICATION NUMBER: 60/426,137
;  PRIOR FILING DATE: 2002-11-14
;  NUMBER OF SEQ ID NOS: 1591911
;  SOFTWARE: Proprietary
; SEQ ID NO 440242
;   LENGTH: 19
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-11-101-244-440242

  Query Match             72.0%;  Score 14.4;  DB 1;  Length 19;
  Best Local Similarity   75.0%;  Pred. No. 10;
  Matches   12;  Conservative    3;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          5 ATGGTCACATGGATGA 20
              | ||:||||:|||:||
Db          4 AAGGUCACAUGGAUGA 19


RESULT 14
US-11-083-784-15285/c
; Sequence 15285, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
;  APPLICANT: Dharmacon, Inc.
;  APPLICANT:  Khvorova, Anastasia
;  APPLICANT:  Reynolds, Angela
;  APPLICANT:  Leake, Devin
;  APPLICANT:  Marshall, William
;  APPLICANT:  Scaringe, Stephen
;  TITLE OF INVENTION: Functional and Hyperfunctional siRNA
;  FILE REFERENCE: 13499US
;  CURRENT APPLICATION NUMBER: US/11/083,784
;  CURRENT FILING DATE:  2005-03-18
;  PRIOR APPLICATION NUMBER: US/10/714,333
;  PRIOR FILING DATE: 2003-11-14
;  PRIOR APPLICATION NUMBER: 60/502,050
;  PRIOR FILING DATE: 2003-09-10
;  PRIOR APPLICATION NUMBER: 60/426,137
;  PRIOR FILING DATE: 2002-11-14
;  NUMBER OF SEQ ID NOS: 1591911
;  SOFTWARE: Proprietary
; SEQ ID NO 15285
;   LENGTH: 19
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-11-083-784-15285

  Query Match             69.0%;  Score 13.8;  DB 1;  Length 19;
  Best Local Similarity   88.2%;  Pred. No. 12;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          3 TCATGGTCACATGGATG 19
              |||||||||  ||||||
Db         18 TCATGGTCAGGTGGATG 2


RESULT 15
US-11-083-784-144519
; Sequence 144519, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
;  APPLICANT: Dharmacon, Inc.
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;  APPLICANT:  Khvorova, Anastasia
;  APPLICANT:  Reynolds, Angela
;  APPLICANT:  Leake, Devin
;  APPLICANT:  Marshall, William
;  APPLICANT:  Scaringe, Stephen
;  TITLE OF INVENTION: Functional and Hyperfunctional siRNA
;  FILE REFERENCE: 13499US
;  CURRENT APPLICATION NUMBER: US/11/083,784
;  CURRENT FILING DATE:  2005-03-18
;  PRIOR APPLICATION NUMBER: US/10/714,333
;  PRIOR FILING DATE: 2003-11-14
;  PRIOR APPLICATION NUMBER: 60/502,050
;  PRIOR FILING DATE: 2003-09-10
;  PRIOR APPLICATION NUMBER: 60/426,137
;  PRIOR FILING DATE: 2002-11-14
;  NUMBER OF SEQ ID NOS: 1591911
;  SOFTWARE: Proprietary
; SEQ ID NO 144519
;   LENGTH: 19
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-11-083-784-144519

  Query Match             69.0%;  Score 13.8;  DB 1;  Length 19;
  Best Local Similarity   70.6%;  Pred. No. 12;
  Matches   12;  Conservative    3;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 CCTCATGGTCACATGGA 17
              | :|| ||:||||:|||
Db          2 CAUCAGGGUCACAUGGA 18


RESULT 16
US-11-083-784-1218947
; Sequence 1218947, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
;  APPLICANT: Dharmacon, Inc.
;  APPLICANT:  Khvorova, Anastasia
;  APPLICANT:  Reynolds, Angela
;  APPLICANT:  Leake, Devin
;  APPLICANT:  Marshall, William
;  APPLICANT:  Scaringe, Stephen
;  TITLE OF INVENTION: Functional and Hyperfunctional siRNA
;  FILE REFERENCE: 13499US
;  CURRENT APPLICATION NUMBER: US/11/083,784
;  CURRENT FILING DATE:  2005-03-18
;  PRIOR APPLICATION NUMBER: US/10/714,333
;  PRIOR FILING DATE: 2003-11-14
;  PRIOR APPLICATION NUMBER: 60/502,050
;  PRIOR FILING DATE: 2003-09-10
;  PRIOR APPLICATION NUMBER: 60/426,137
;  PRIOR FILING DATE: 2002-11-14
;  NUMBER OF SEQ ID NOS: 1591911
;  SOFTWARE: Proprietary
; SEQ ID NO 1218947
;   LENGTH: 19
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-11-083-784-1218947

  Query Match             69.0%;  Score 13.8;  DB 1;  Length 19;
  Best Local Similarity   64.7%;  Pred. No. 12;
  Matches   11;  Conservative    4;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 CCTCATGGTCACATGGA 17
              ||:||:||: |||: ||
Db          3 CCUCAUGGUGACAUUGA 19


RESULT 17
US-11-101-244-15285/c
; Sequence 15285, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
;  APPLICANT: Dharmacon, Inc.
;  APPLICANT:  Khvorova, Anastasia
;  APPLICANT:  Reynolds, Angela
;  APPLICANT:  Leake, Devin
;  APPLICANT:  Marshall, William
;  APPLICANT:  Scaringe, Stephen
;  TITLE OF INVENTION: Functional and Hyperfunctional siRNA
;  FILE REFERENCE: 13499US
;  CURRENT APPLICATION NUMBER: US/11/101,244
;  CURRENT FILING DATE:  2005-04-07
;  PRIOR APPLICATION NUMBER: 60/502,050
;  PRIOR FILING DATE: 2003-09-10
;  PRIOR APPLICATION NUMBER: 60/426,137
;  PRIOR FILING DATE: 2002-11-14
;  NUMBER OF SEQ ID NOS: 1591911
;  SOFTWARE: Proprietary
; SEQ ID NO 15285
;   LENGTH: 19
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-11-101-244-15285

  Query Match             69.0%;  Score 13.8;  DB 1;  Length 19;
  Best Local Similarity   88.2%;  Pred. No. 12;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          3 TCATGGTCACATGGATG 19
              |||||||||  ||||||
Db         18 TCATGGTCAGGTGGATG 2


RESULT 18
US-11-101-244-144519
; Sequence 144519, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
;  APPLICANT: Dharmacon, Inc.
;  APPLICANT:  Khvorova, Anastasia
;  APPLICANT:  Reynolds, Angela
;  APPLICANT:  Leake, Devin
;  APPLICANT:  Marshall, William
;  APPLICANT:  Scaringe, Stephen
;  TITLE OF INVENTION: Functional and Hyperfunctional siRNA
;  FILE REFERENCE: 13499US
;  CURRENT APPLICATION NUMBER: US/11/101,244
;  CURRENT FILING DATE:  2005-04-07
;  PRIOR APPLICATION NUMBER: 60/502,050
;  PRIOR FILING DATE: 2003-09-10
;  PRIOR APPLICATION NUMBER: 60/426,137
;  PRIOR FILING DATE: 2002-11-14
;  NUMBER OF SEQ ID NOS: 1591911
;  SOFTWARE: Proprietary
; SEQ ID NO 144519
;   LENGTH: 19
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-11-101-244-144519

  Query Match             69.0%;  Score 13.8;  DB 1;  Length 19;
  Best Local Similarity   70.6%;  Pred. No. 12;
  Matches   12;  Conservative    3;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 CCTCATGGTCACATGGA 17
              | :|| ||:||||:|||
Db          2 CAUCAGGGUCACAUGGA 18


RESULT 19
US-11-101-244-1218947
; Sequence 1218947, Application US/11101244
; Publication No. US20050246794A1
```

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; GENERAL INFORMATION:
;  APPLICANT: Dharmacon, Inc.
;  APPLICANT:  Khvorova, Anastasia
;  APPLICANT:  Reynolds, Angela
;  APPLICANT:  Leake, Devin
;  APPLICANT:  Marshall, William
;  APPLICANT:  Scaringe, Stephen
;  TITLE OF INVENTION: Functional and Hyperfunctional siRNA
;  FILE REFERENCE: 13499US
;  CURRENT APPLICATION NUMBER: US/11/101,244
;  CURRENT FILING DATE:  2005-04-07
;  PRIOR APPLICATION NUMBER: 60/502,050
;  PRIOR FILING DATE: 2003-09-10
;  PRIOR APPLICATION NUMBER: 60/426,137
;  PRIOR FILING DATE: 2002-11-14
;  NUMBER OF SEQ ID NOS: 1591911
;  SOFTWARE: Proprietary
; SEQ ID NO 1218947
;   LENGTH: 19
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-11-101-244-1218947

  Query Match             69.0%;  Score 13.8;  DB 1;  Length 19;
  Best Local Similarity   64.7%;  Pred. No. 12;
  Matches   11;  Conservative    4;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 CCTCATGGTCACATGGA 17
              ||:||:||: |||: ||
Db          3 CCUCAUGGUGACAUUGA 19


RESULT 20
US-11-083-784-155627/c
; Sequence 155627, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
;  APPLICANT: Dharmacon, Inc.
;  APPLICANT:  Khvorova, Anastasia
;  APPLICANT:  Reynolds, Angela
;  APPLICANT:  Leake, Devin
;  APPLICANT:  Marshall, William
;  APPLICANT:  Scaringe, Stephen
;  TITLE OF INVENTION: Functional and Hyperfunctional siRNA
;  FILE REFERENCE: 13499US
;  CURRENT APPLICATION NUMBER: US/11/083,784
;  CURRENT FILING DATE:  2005-03-18
;  PRIOR APPLICATION NUMBER: US/10/714,333
;  PRIOR FILING DATE: 2003-11-14
;  PRIOR APPLICATION NUMBER: 60/502,050
;  PRIOR FILING DATE: 2003-09-10
;  PRIOR APPLICATION NUMBER: 60/426,137
;  PRIOR FILING DATE: 2002-11-14
;  NUMBER OF SEQ ID NOS: 1591911
;  SOFTWARE: Proprietary
; SEQ ID NO 155627
;   LENGTH: 19
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-11-083-784-155627

  Query Match             67.0%;  Score 13.4;  DB 1;  Length 19;
  Best Local Similarity   93.3%;  Pred. No. 13;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          6 TGGTCACATGGATGA 20
              |||| ||||||||||
Db         17 TGGTTACATGGATGA 3


RESULT 21
US-11-083-784-155645/c
; Sequence 155645, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
;  APPLICANT: Dharmacon, Inc.
;  APPLICANT:  Khvorova, Anastasia
;  APPLICANT:  Reynolds, Angela
;  APPLICANT:  Leake, Devin
;  APPLICANT:  Marshall, William
;  APPLICANT:  Scaringe, Stephen
;  TITLE OF INVENTION: Functional and Hyperfunctional siRNA
;  FILE REFERENCE: 13499US
;  CURRENT APPLICATION NUMBER: US/11/083,784
;  CURRENT FILING DATE:  2005-03-18
;  PRIOR APPLICATION NUMBER: US/10/714,333
;  PRIOR FILING DATE: 2003-11-14
;  PRIOR APPLICATION NUMBER: 60/502,050
;  PRIOR FILING DATE: 2003-09-10
;  PRIOR APPLICATION NUMBER: 60/426,137
;  PRIOR FILING DATE: 2002-11-14
;  NUMBER OF SEQ ID NOS: 1591911
;  SOFTWARE: Proprietary
; SEQ ID NO 155645
;   LENGTH: 19
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-11-083-784-155645

  Query Match             67.0%;  Score 13.4;  DB 1;  Length 19;
  Best Local Similarity   93.3%;  Pred. No. 13;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          6 TGGTCACATGGATGA 20
              |||| ||||||||||
Db         19 TGGTTACATGGATGA 5


RESULT 22
US-11-083-784-943972
; Sequence 943972, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
;  APPLICANT: Dharmacon, Inc.
;  APPLICANT:  Khvorova, Anastasia
;  APPLICANT:  Reynolds, Angela
;  APPLICANT:  Leake, Devin
;  APPLICANT:  Marshall, William
;  APPLICANT:  Scaringe, Stephen
;  TITLE OF INVENTION: Functional and Hyperfunctional siRNA
;  FILE REFERENCE: 13499US
;  CURRENT APPLICATION NUMBER: US/11/083,784
;  CURRENT FILING DATE:  2005-03-18
;  PRIOR APPLICATION NUMBER: US/10/714,333
;  PRIOR FILING DATE: 2003-11-14
;  PRIOR APPLICATION NUMBER: 60/502,050
;  PRIOR FILING DATE: 2003-09-10
;  PRIOR APPLICATION NUMBER: 60/426,137
;  PRIOR FILING DATE: 2002-11-14
;  NUMBER OF SEQ ID NOS: 1591911
;  SOFTWARE: Proprietary
; SEQ ID NO 943972
;   LENGTH: 19
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-11-083-784-943972

  Query Match             67.0%;  Score 13.4;  DB 1;  Length 19;
  Best Local Similarity   66.7%;  Pred. No. 13;
  Matches   10;  Conservative    4;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          6 TGGTCACATGGATGA 20
              :||:| ||:|||:||
Db          5 UGGUCCCAUGGAUGA 19
```

```
RESULT 23
US-11-083-784-1009396/c
; Sequence 1009396, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
;  APPLICANT: Dharmacon, Inc.
;  APPLICANT:  Khvorova, Anastasia
;  APPLICANT:  Reynolds, Angela
;  APPLICANT:  Leake, Devin
;  APPLICANT:  Marshall, William
;  APPLICANT:  Scaringe, Stephen
;  TITLE OF INVENTION: Functional and Hyperfunctional siRNA
;  FILE REFERENCE: 13499US
;  CURRENT APPLICATION NUMBER: US/11/083,784
;  CURRENT FILING DATE:  2005-03-18
;  PRIOR APPLICATION NUMBER: US/10/714,333
;  PRIOR FILING DATE: 2003-11-14
;  PRIOR APPLICATION NUMBER: 60/502,050
;  PRIOR FILING DATE: 2003-09-10
;  PRIOR APPLICATION NUMBER: 60/426,137
;  PRIOR FILING DATE: 2002-11-14
;  NUMBER OF SEQ ID NOS: 1591911
;  SOFTWARE: Proprietary
; SEQ ID NO 1009396
;   LENGTH: 19
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-11-083-784-1009396

  Query Match             67.0%;  Score 13.4;  DB 1;  Length 19;
  Best Local Similarity   93.3%;  Pred. No. 13;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 CCTCATGGTCACATG 15
              ||||| |||||||||
Db         15 CCTCAAGGTCACATG 1


RESULT 24
US-11-083-784-1224506
; Sequence 1224506, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
;  APPLICANT: Dharmacon, Inc.
;  APPLICANT:  Khvorova, Anastasia
;  APPLICANT:  Reynolds, Angela
;  APPLICANT:  Leake, Devin
;  APPLICANT:  Marshall, William
;  APPLICANT:  Scaringe, Stephen
;  TITLE OF INVENTION: Functional and Hyperfunctional siRNA
;  FILE REFERENCE: 13499US
;  CURRENT APPLICATION NUMBER: US/11/083,784
;  CURRENT FILING DATE:  2005-03-18
;  PRIOR APPLICATION NUMBER: US/10/714,333
;  PRIOR FILING DATE: 2003-11-14
;  PRIOR APPLICATION NUMBER: 60/502,050
;  PRIOR FILING DATE: 2003-09-10
;  PRIOR APPLICATION NUMBER: 60/426,137
;  PRIOR FILING DATE: 2002-11-14
;  NUMBER OF SEQ ID NOS: 1591911
;  SOFTWARE: Proprietary
; SEQ ID NO 1224506
;   LENGTH: 19
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-11-083-784-1224506

  Query Match             67.0%;  Score 13.4;  DB 1;  Length 19;
  Best Local Similarity   66.7%;  Pred. No. 13;
  Matches   10;  Conservative    4;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          6 TGGTCACATGGATGA 20
              :||: |||:|||:||
Db          2 UGGUUACAUGGAUGA 16


RESULT 25
US-11-101-244-155627/c
; Sequence 155627, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
;  APPLICANT: Dharmacon, Inc.
;  APPLICANT:  Khvorova, Anastasia
;  APPLICANT:  Reynolds, Angela
;  APPLICANT:  Leake, Devin
;  APPLICANT:  Marshall, William
;  APPLICANT:  Scaringe, Stephen
;  TITLE OF INVENTION: Functional and Hyperfunctional siRNA
;  FILE REFERENCE: 13499US
;  CURRENT APPLICATION NUMBER: US/11/101,244
;  CURRENT FILING DATE:  2005-04-07
;  PRIOR APPLICATION NUMBER: 60/502,050
;  PRIOR FILING DATE: 2003-09-10
;  PRIOR APPLICATION NUMBER: 60/426,137
;  PRIOR FILING DATE: 2002-11-14
;  NUMBER OF SEQ ID NOS: 1591911
;  SOFTWARE: Proprietary
; SEQ ID NO 155627
;   LENGTH: 19
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-11-101-244-155627

  Query Match             67.0%;  Score 13.4;  DB 1;  Length 19;
  Best Local Similarity   93.3%;  Pred. No. 13;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          6 TGGTCACATGGATGA 20
              |||| ||||||||||
Db         17 TGGTTACATGGATGA 3


RESULT 26
US-11-101-244-155645/c
; Sequence 155645, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
;  APPLICANT: Dharmacon, Inc.
;  APPLICANT:  Khvorova, Anastasia
;  APPLICANT:  Reynolds, Angela
;  APPLICANT:  Leake, Devin
;  APPLICANT:  Marshall, William
;  APPLICANT:  Scaringe, Stephen
;  TITLE OF INVENTION: Functional and Hyperfunctional siRNA
;  FILE REFERENCE: 13499US
;  CURRENT APPLICATION NUMBER: US/11/101,244
;  CURRENT FILING DATE:  2005-04-07
;  PRIOR APPLICATION NUMBER: 60/502,050
;  PRIOR FILING DATE: 2003-09-10
;  PRIOR APPLICATION NUMBER: 60/426,137
;  PRIOR FILING DATE: 2002-11-14
;  NUMBER OF SEQ ID NOS: 1591911
;  SOFTWARE: Proprietary
; SEQ ID NO 155645
;   LENGTH: 19
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-11-101-244-155645

  Query Match             67.0%;  Score 13.4;  DB 1;  Length 19;
  Best Local Similarity   93.3%;  Pred. No. 13;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          6 TGGTCACATGGATGA 20
              |||| ||||||||||
Db         19 TGGTTACATGGATGA 5
```

```
RESULT 27
US-11-101-244-943972
; Sequence 943972, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
;  APPLICANT: Dharmacon, Inc.
;  APPLICANT:  Khvorova, Anastasia
;  APPLICANT:  Reynolds, Angela
;  APPLICANT:  Leake, Devin
;  APPLICANT:  Marshall, William
;  APPLICANT:  Scaringe, Stephen
;  TITLE OF INVENTION: Functional and Hyperfunctional siRNA
;  FILE REFERENCE: 13499US
;  CURRENT APPLICATION NUMBER: US/11/101,244
;  CURRENT FILING DATE:  2005-04-07
;  PRIOR APPLICATION NUMBER: 60/502,050
;  PRIOR FILING DATE: 2003-09-10
;  PRIOR APPLICATION NUMBER: 60/426,137
;  PRIOR FILING DATE: 2002-11-14
;  NUMBER OF SEQ ID NOS: 1591911
;  SOFTWARE: Proprietary
; SEQ ID NO 943972
;   LENGTH: 19
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-11-101-244-943972

  Query Match             67.0%;  Score 13.4;  DB 1;  Length 19;
  Best Local Similarity   66.7%;  Pred. No. 13;
  Matches   10;  Conservative    4;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          6 TGGTCACATGGATGA 20
              :||:| ||:|||:||
Db          5 UGGUCCCAUGGAUGA 19


RESULT 28
US-11-101-244-1009396/c
; Sequence 1009396, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
;  APPLICANT: Dharmacon, Inc.
;  APPLICANT:  Khvorova, Anastasia
;  APPLICANT:  Reynolds, Angela
;  APPLICANT:  Leake, Devin
;  APPLICANT:  Marshall, William
;  APPLICANT:  Scaringe, Stephen
;  TITLE OF INVENTION: Functional and Hyperfunctional siRNA
;  FILE REFERENCE: 13499US
;  CURRENT APPLICATION NUMBER: US/11/101,244
;  CURRENT FILING DATE:  2005-04-07
;  PRIOR APPLICATION NUMBER: 60/502,050
;  PRIOR FILING DATE: 2003-09-10
;  PRIOR APPLICATION NUMBER: 60/426,137
;  PRIOR FILING DATE: 2002-11-14
;  NUMBER OF SEQ ID NOS: 1591911
;  SOFTWARE: Proprietary
; SEQ ID NO 1009396
;   LENGTH: 19
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-11-101-244-1009396

  Query Match             67.0%;  Score 13.4;  DB 1;  Length 19;
  Best Local Similarity   93.3%;  Pred. No. 13;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 CCTCATGGTCACATG 15
              ||||| |||||||||
Db         15 CCTCAAGGTCACATG 1


RESULT 29
US-11-101-244-1224506
; Sequence 1224506, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
;  APPLICANT: Dharmacon, Inc.
;  APPLICANT:  Khvorova, Anastasia
;  APPLICANT:  Reynolds, Angela
;  APPLICANT:  Leake, Devin
;  APPLICANT:  Marshall, William
;  APPLICANT:  Scaringe, Stephen
;  TITLE OF INVENTION: Functional and Hyperfunctional siRNA
;  FILE REFERENCE: 13499US
;  CURRENT APPLICATION NUMBER: US/11/101,244
;  CURRENT FILING DATE:  2005-04-07
;  PRIOR APPLICATION NUMBER: 60/502,050
;  PRIOR FILING DATE: 2003-09-10
;  PRIOR APPLICATION NUMBER: 60/426,137
;  PRIOR FILING DATE: 2002-11-14
;  NUMBER OF SEQ ID NOS: 1591911
;  SOFTWARE: Proprietary
; SEQ ID NO 1224506
;   LENGTH: 19
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-11-101-244-1224506

  Query Match             67.0%;  Score 13.4;  DB 1;  Length 19;
  Best Local Similarity   66.7%;  Pred. No. 13;
  Matches   10;  Conservative    4;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          6 TGGTCACATGGATGA 20
              :||: |||:|||:||
Db          2 UGGUUACAUGGAUGA 16


RESULT 30
US-09-866-108-7612/c
; Sequence 7612, Application US/09866108
; Patent No. US20020048800A1
; GENERAL INFORMATION:
;  APPLICANT: GU, Yizhong
;  APPLICANT:  JI, Yonggang
;  APPLICANT:  PENN, Sharron G.
;  APPLICANT:  HANZEL, David K.
;  APPLICANT:  RANK, David R.
;  APPLICANT:  CHEN, Wensheng
;  APPLICANT:  SHANNON, Mark
;  TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
;  FILE REFERENCE: AEOMICA-7
;  CURRENT APPLICATION NUMBER: US/09/866,108
;  CURRENT FILING DATE:  2001-05-25
;  PRIOR APPLICATION NUMBER: US 60/207,456
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: GB 24263.6
;  PRIOR FILING DATE: 2000-10-04
;  PRIOR APPLICATION NUMBER: US 60/236,359
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: PCT/US01/00666
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00667
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00664
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00669
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00665
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00668
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00663
;  PRIOR FILING DATE: 2001-01-30
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;  PRIOR APPLICATION NUMBER: PCT/US01/00662
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00661
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00670
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: US 60/234,687
;  PRIOR FILING DATE: 2000-09-21
;  PRIOR APPLICATION NUMBER: US 60/266,860
;  PRIOR FILING DATE: 2001-02-05
;  NUMBER OF SEQ ID NOS: 15752
;  SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 7612
;   LENGTH: 17
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-866-108-7612

  Query Match             61.0%;  Score 12.2;  DB 1;  Length 17;
  Best Local Similarity   82.4%;  Pred. No. 15;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 CCTCATGGTCACATGGA 17
              ||||| ||||||| | |
Db         17 CCTCAAGGTCACAGGTA 1


RESULT 31
US-10-723-361-7612/c
; Sequence 7612, Application US/10723361
; Publication No. US20040137589A1
; GENERAL INFORMATION:
;  APPLICANT: GU, Yizhong
;  APPLICANT:  JI, Yonggang
;  APPLICANT:  PENN, Sharron G.
;  APPLICANT:  HANZEL, David K.
;  APPLICANT:  RANK, David R.
;  APPLICANT:  CHEN, Wensheng
;  APPLICANT:  SHANNON, Mark
;  TITLE OF INVENTION: HUMAN MYOSIN-LIKE POLYPEPTIDE EXPRESSED PREDOMINANTLY IN HEART AN
;  FILE REFERENCE: PB0105
;  CURRENT APPLICATION NUMBER: US/10/723,361
;  CURRENT FILING DATE:  2003-11-26
;  PRIOR APPLICATION NUMBER: US 09/866,108
;  PRIOR FILING DATE: 2001-05-25
;  PRIOR APPLICATION NUMBER: US 60/207,456
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: GB 24263.6
;  PRIOR FILING DATE: 2000-10-04
;  PRIOR APPLICATION NUMBER: US 60/236,359
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: PCT/US01/00666
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00667
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00664
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00669
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00665
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00668
;  PRIOR FILING DATE: 2001-01-30
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 15755
;  SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 7612
;   LENGTH: 17
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-723-361-7612

  Query Match             61.0%;  Score 12.2;  DB 1;  Length 17;
  Best Local Similarity   82.4%;  Pred. No. 15;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 CCTCATGGTCACATGGA 17
              ||||| ||||||| | |
Db         17 CCTCAAGGTCACAGGTA 1


RESULT 32
US-09-916-466-30
; Sequence 30, Application US/09916466
; Publication No. US20030064945A1
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceuticals, Inc.
;  APPLICANT:  Akhtar, Saghir
;  APPLICANT:  McSwiggen, Jim
;  TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or conditions Relat
;  TITLE OF INVENTION:  Levels of Epidermal Growth Factor Receptors
;  FILE REFERENCE: MBHB00-958-J (400/032)
;  CURRENT APPLICATION NUMBER: US/09/916,466
;  CURRENT FILING DATE:  2001-07-25
;  NUMBER OF SEQ ID NOS: 446
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 30
;   LENGTH: 15
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-09-916-466-30

  Query Match             57.0%;  Score 11.4;  DB 1;  Length 15;
  Best Local Similarity   61.5%;  Pred. No. 15;
  Matches    8;  Conservative    4;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 TCATGGTCACATG 15
              :||:||:|| |:|
Db          1 UCAUGGUCAAAUG 13


RESULT 33
US-10-277-494-30
; Sequence 30, Application US/10277494
; Publication No. US20030186909A1
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceuticals, Inc.
;  APPLICANT:  McSwiggen, Jim
;  TITLE OF INVENTION: Nucleic Acid Treatment of Diseases or conditions Related To Level
;  TITLE OF INVENTION:  Epidermal Growth Factor Receptors
;  FILE REFERENCE: MBHB00-958-K (400/064)
;  CURRENT APPLICATION NUMBER: US/10/277,494
;  CURRENT FILING DATE:  2002-10-21
;  NUMBER OF SEQ ID NOS: 446
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 30
;   LENGTH: 15
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-10-277-494-30

  Query Match             57.0%;  Score 11.4;  DB 1;  Length 15;
  Best Local Similarity   61.5%;  Pred. No. 15;
  Matches    8;  Conservative    4;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 TCATGGTCACATG 15
              :||:||:|| |:|
Db          1 UCAUGGUCAAAUG 13


RESULT 34
US-10-257-017B-228161
; Sequence 228161, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
;  APPLICANT: Alexander Olek
```

```
;  APPLICANT:  Christian Piepenbrock
;  APPLICANT:  Kurt Berlin
;  TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
;  TITLE OF INVENTION:  methylations
;  FILE REFERENCE: E01/1193/WO
;  CURRENT APPLICATION NUMBER: US/10/257,017B
;  CURRENT FILING DATE:  2002-10-07
;  PRIOR APPLICATION NUMBER: DE 10019173.8
;  PRIOR FILING DATE: 2000-04-07
;  NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 228161
;   LENGTH: 13
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0055641
US-10-257-017B-228161

  Query Match             49.0%;  Score 9.8;  DB 1;  Length 13;
  Best Local Similarity   84.6%;  Pred. No. 17;
  Matches   11;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          8 GTCACATGGATGA 20
              || || |||||||
Db          1 GTTACGTGGATGA 13


RESULT 35
US-10-257-017B-228162/c
; Sequence 228162, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
;  APPLICANT: Alexander Olek
;  APPLICANT:  Christian Piepenbrock
;  APPLICANT:  Kurt Berlin
;  TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
;  TITLE OF INVENTION:  methylations
;  FILE REFERENCE: E01/1193/WO
;  CURRENT APPLICATION NUMBER: US/10/257,017B
;  CURRENT FILING DATE:  2002-10-07
;  PRIOR APPLICATION NUMBER: DE 10019173.8
;  PRIOR FILING DATE: 2000-04-07
;  NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 228162
;   LENGTH: 13
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0055641
US-10-257-017B-228162

  Query Match             49.0%;  Score 9.8;  DB 1;  Length 13;
  Best Local Similarity   84.6%;  Pred. No. 17;
  Matches   11;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          8 GTCACATGGATGA 20
              || || |||||||
Db         13 GTTACGTGGATGA 1


RESULT 36
US-10-257-017B-245261
; Sequence 245261, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
;  APPLICANT: Alexander Olek
;  APPLICANT:  Christian Piepenbrock
;  APPLICANT:  Kurt Berlin
;  TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
;  TITLE OF INVENTION:  methylations
;  FILE REFERENCE: E01/1193/WO
;  CURRENT APPLICATION NUMBER: US/10/257,017B
;  CURRENT FILING DATE:  2002-10-07
;  PRIOR APPLICATION NUMBER: DE 10019173.8
;  PRIOR FILING DATE: 2000-04-07
;  NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 245261
;   LENGTH: 13
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0059887
US-10-257-017B-245261

  Query Match             49.0%;  Score 9.8;  DB 1;  Length 13;
  Best Local Similarity   84.6%;  Pred. No. 17;
  Matches   11;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          6 TGGTCACATGGAT 18
              |||| || |||||
Db          1 TGGTAACGTGGAT 13


RESULT 37
US-10-257-017B-245262/c
; Sequence 245262, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
;  APPLICANT: Alexander Olek
;  APPLICANT:  Christian Piepenbrock
;  APPLICANT:  Kurt Berlin
;  TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
;  TITLE OF INVENTION:  methylations
;  FILE REFERENCE: E01/1193/WO
;  CURRENT APPLICATION NUMBER: US/10/257,017B
;  CURRENT FILING DATE:  2002-10-07
;  PRIOR APPLICATION NUMBER: DE 10019173.8
;  PRIOR FILING DATE: 2000-04-07
;  NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 245262
;   LENGTH: 13
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0059887
US-10-257-017B-245262

  Query Match             49.0%;  Score 9.8;  DB 1;  Length 13;
  Best Local Similarity   84.6%;  Pred. No. 17;
  Matches   11;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          6 TGGTCACATGGAT 18
              |||| || |||||
Db         13 TGGTAACGTGGAT 1


Search completed: June 13, 2006, 15:50:13
Job time : 0.001 secs
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GenCore version 5.1.9

OM nucleic - nucleic search, using sw model

Run on: June 13, 2006, 15:46:01 ; Search time 0.001 Seconds
(without alignments)
46.240 Million cell updates/sec

Title: US-10-719-370A-446
Perfect score: 20
Sequence: 1 cctcatggtcacatggatga 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 0.5

Searched: 80 seqs, 1156 residues

Total number of hits satisfying chosen parameters: 160

Minimum DB seq length: 12
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 80 summaries

Database : us-10-719-370a-446.sl.rng4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	20	100.0	20	1	ADT78875	Antisense oligonuc
	2	19	95.0	20	1	ADT78876	Antisense oligonuc
	3	19	95.0	20	1	ADT78571	HIF1alpha cDNA, an
	4	18	90.0	20	1	ADT78881	Antisense oligonuc
	5	18	90.0	20	1	ADT78874	Antisense oligonuc
	6	17	85.0	20	1	ADQ88746	Human HIF-1 antise
	7	17	85.0	20	1	ADT78880	Antisense oligonuc
	8	16.8	84.0	20	1	ADT78872	Antisense oligonuc
	9	16	80.0	20	1	ADT78877	Antisense oligonuc
	10	15.8	79.0	20	1	ADT78879	Antisense oligonuc
	11	14.8	74.0	19	1	AAV13322	Sense primer Exon
	12	14	70.0	19	1	ADZ58131	Antisense siRNA ol
c	13	14	70.0	19	1	ADZ57911	Sense siRNA oligo
c	14	12.8	64.0	17	1	ABT38435	Tumour suppression
c	15	12.8	64.0	18	1	ADW14071	KCNMA1 exon 1B sen
c	16	12.2	61.0	17	1	ABN07620	Human GDMLP-1 17-m
	17	12.2	61.0	17	1	ACN12001	WNV minus strand I
c	18	12.2	61.0	17	1	ACN70710	Human GDMLP-1 prob
c	19	11.8	59.0	15	1	AAF51883	IGF-I oligonucleot
c	20	11.8	59.0	15	1	AAF51884	IGF-I oligonucleot
c	21	11.8	59.0	16	1	ADZ59539	Hyperparathyroidis
c	22	11.8	59.0	16	1	ADZ59706	Hyperparathyroidis
	23	11.4	57.0	15	1	ADG13603	Human HER1-4 hamme
c	24	11.4	57.0	16	1	ADM69289	Plant gene polymor
c	25	11.2	56.0	16	1	ADR74253	Common primer B fo
	26	11	55.0	15	1	ABK09404	Human NPR1 gene al
	27	11	55.0	15	1	ACL73850	SARS coronavirus r
	28	11	55.0	15	1	ACL73880	SARS coronavirus r
	29	11	55.0	15	1	ACL73792	SARS coronavirus r
	30	10.8	54.0	14	1	ADL96404	Acute myeloid leuk
	31	10.8	54.0	15	1	AAX31458	Tag sequence of a
c	32	10.8	54.0	15	1	AAF51885	IGF-I oligonucleot
c	33	10.8	54.0	15	1	AAF51882	IGF-I oligonucleot
	34	10.8	54.0	15	1	ABK32412	Human colon cancer
c	35	10.4	52.0	14	1	ADQ82962	Extended hairpin t
c	36	10.4	52.0	14	1	ADQ82964	Extended hairpin t
c	37	10	50.0	14	1	AAT36745	Antisense oligonuc
c	38	10	50.0	14	1	AAH89017	Human polymorphic
c	39	9.8	49.0	13	1	ABH45285	Oligonucleotide SE
	40	9.8	49.0	13	1	ABH45284	Oligonucleotide SE
c	41	9.8	49.0	13	1	ABH28185	Oligonucleotide SE
	42	9.8	49.0	13	1	ABH28184	Oligonucleotide SE
c	43	9.8	49.0	14	1	AAN70553	Sequence of probe
c	44	9.4	47.0	13	1	AAX19072	Human PPAR-gamma-3
	45	9.4	47.0	13	1	ADZ24722	Human SNP detectio
	46	9.4	47.0	13	1	AED86939	Polyamide-binding
c	47	9.4	47.0	13	1	AED86940	Polyamide-binding
c	48	9	45.0	12	1	AAQ88597	Human mitochondria
	49	9	45.0	12	1	AAV32269	Random primed reve
c	50	8.8	44.0	12	1	AAH23540	Antibacterial pept
	51	8.8	44.0	12	1	ABH82120	Oligonucleotide pr
	52	8.8	44.0	12	1	ABI08296	Oligonucleotide pr
	53	8.8	44.0	12	1	ADW11578	siRNA production-r
	54	8.4	42.0	12	1	AAQ24034	Herpesvirus inhibi
c	55	8.4	42.0	12	1	AAQ30497	Adenovirus major l
c	56	8.4	42.0	12	1	AAQ52946	Herpes simplex vir
c	57	8.4	42.0	12	1	AAZ59958	Adenovirus Ad5 maj
	58	8.4	42.0	12	1	AAA30866	Fragment of a plas
c	59	8.4	42.0	12	1	ABI48155	Oligonucleotide pr
	60	8.4	42.0	12	1	ABI35107	Oligonucleotide pr
	61	8.4	42.0	12	1	ABI72389	Oligonucleotide pr
c	62	8.4	42.0	12	1	ABH84083	Oligonucleotide pr
	63	8.4	42.0	12	1	ABI04761	Oligonucleotide pr
	64	8.4	42.0	12	1	ABH67680	Oligonucleotide pr
c	65	8.4	42.0	12	1	ABI08303	Oligonucleotide pr
c	66	8.4	42.0	12	1	ABI29750	Oligonucleotide pr
	67	8.4	42.0	12	1	AAH49257	PNA-forming oligon
	68	8.4	42.0	12	1	AAH49256	PNA-forming oligon
	69	8.4	42.0	12	1	AAH49260	PNA-forming oligon
	70	8.4	42.0	12	1	AAH49261	PNA-forming oligon
	71	8.4	42.0	12	1	AAH49259	PNA-forming oligon
	72	8.4	42.0	12	1	AAH49258	PNA-forming oligon
c	73	8.4	42.0	12	1	ABA82718	Human protective D
	74	8.4	42.0	12	1	ABK72560	Human OPA1 gene, e
c	75	8.4	42.0	12	1	ABA01332	HIV-1 rev oligonuc
	76	8.4	42.0	12	1	AAK98610	Modified peptide n
	77	8.4	42.0	12	1	ABA97503	Peptide nucleic ac
c	78	8.4	42.0	12	1	ADM56294	Mouse SLC26A6 anio
	79	8.4	42.0	12	1	ADQ29965	Rat VR1 exon 1d tr
c	80	8.4	42.0	12	1	AEF80873	MLTF/USF promoter

ALIGNMENTS

RESULT 1
ADT78875
ID ADT78875 standard; DNA; 20 BP.
XX
AC ADT78875;
XX
DT 27-JAN-2005 (first entry)
XX
DE Antisense oligonucleotide (ISIS 330449) for human HIF1alpha.
XX
KW Antisense therapy; human; hypoxia-inducible factor 1 alpha;
KW hypoxia-inducible factor 2 alpha; HIF1alpha; HIF2alpha;
KW hyperproliferative disorder; cancer; p53; angiogenic disorder;
KW eye disorder; tumour; hyperplasia; pulmonary fibrosis; angiogenesis;
KW psoriasis; atherosclerosis; smooth muscle cell proliferation;
KW blood vessel; restenosis; angioplasty; cytostatic; angiogenesis;
KW ophthalmological; antiinflammatory; respiratory; vasotropic; ss.
XX
OS Homo sapiens.
XX
PN US2004220393-A1.

XX
PD 04-NOV-2004.
XX
PF 21-NOV-2003; 2003US-00719370.
XX
PR 23-NOV-2002; 2002US-00304126.
XX
PA (WARD/) WARD D T.
PA (DOBI/) DOBIE K W.
PA (MARC/) MARCUSSON E G.
PA (FREI/) FREIER S M.
XX
PI Ward DT, Dobie KW, Marcusson EG, Freier SM;
XX
DR WPI; 2004-774955/76.
XX
PT New antisense compound which inhibits the expression of hypoxia-inducible
PT factor 1 alpha (HIF1 alpha) and/or HIF2 alpha, useful for treating
PT hyperproliferative disorder, e.g. cancer carrying a p53 mutation.
XX
PS Claim 92; SEQ ID NO 446; 195pp; English.
XX
CC The present invention relates to antisense compounds targeted to nucleic
CC acids encoding hypoxia-inducible factor 1 alpha (HIF1alpha) and/or
CC hypoxia-inducible factor 2 alpha (HIF2alpha). The antisense compound
CC comprises an antisense oligonucleotide that specifically hybridises with
CC the nucleic acid and inhibits the expression of HIF1alpha and/or
CC HIF2alpha. The antisense oligonucleotide is a chimeric oligonucleotide.
CC The antisense oligonucleotide comprises at least one modified
CC internucleoside linkage, preferably a phosphorothioate linkage. It also
CC comprises at least one modified sugar moiety, preferably a 2'-O-
CC methoxyethyl (2'-MOE) sugar moiety. The antisense oligonucleotide further
CC comprises at least one modified nucleobase, preferably a 5-
CC methylcytosine. The antisense oligonucleotides are useful for the
CC treatment of diseases such as hyperproliferative disorders, e.g. cancer,
CC preferably a cancer carrying a p53 mutation, or an angiogenic disorder
CC that affects the eye. The compound is also useful for treating tumours,
CC hyperplasias, pulmonary fibrosis, angiogenesis, psoriasis,
CC atherosclerosis and smooth muscle cell proliferation in the blood vessels
CC such as stenosis or restenosis following angioplasty. It is also useful
CC in drug discovery and target validation, and can be utilised for
CC diagnostics, therapeutics, prophylaxis and as research reagents and kits.
CC The present sequence represents an oligonucleotide used in the examples
CC of the present invention.
XX
SQ Sequence 20 BP; 5 A; 5 C; 5 G; 5 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTCATGGTCACATGGATGA 20
||||||||||||||||||||
Db 1 CCTCATGGTCACATGGATGA 20

RESULT 2
ADT78876
ID ADT78876 standard; DNA; 20 BP.
XX
AC ADT78876;
XX
DT 27-JAN-2005 (first entry)
XX
DE Antisense oligonucleotide (ISIS 330448) for human HIF1alpha.
XX
KW Antisense therapy; human; hypoxia-inducible factor 1 alpha;
KW hypoxia-inducible factor 2 alpha; HIF1alpha; HIF2alpha;
KW hyperproliferative disorder; cancer; p53; angiogenic disorder;
KW eye disorder; tumour; hyperplasia; pulmonary fibrosis; angiogenesis;
KW psoriasis; atherosclerosis; smooth muscle cell proliferation;
KW blood vessel; restenosis; angioplasty; cytostatic; angiogenesis;
KW ophthalmological; antiinflammatory; respiratory; vasotropic; ss.
XX
OS Homo sapiens.
XX
PN US2004220393-A1.
XX
PD 04-NOV-2004.
XX
PF 21-NOV-2003; 2003US-00719370.
XX
PR 23-NOV-2002; 2002US-00304126.
XX
PA (WARD/) WARD D T.
PA (DOBI/) DOBIE K W.
PA (MARC/) MARCUSSON E G.
PA (FREI/) FREIER S M.
XX
PI Ward DT, Dobie KW, Marcusson EG, Freier SM;
XX
DR WPI; 2004-774955/76.
XX
PT New antisense compound which inhibits the expression of hypoxia-inducible
PT factor 1 alpha (HIF1 alpha) and/or HIF2 alpha, useful for treating
PT hyperproliferative disorder, e.g. cancer carrying a p53 mutation.
XX
PS Claim 92; SEQ ID NO 447; 195pp; English.
XX
CC The present invention relates to antisense compounds targeted to nucleic
CC acids encoding hypoxia-inducible factor 1 alpha (HIF1alpha) and/or
CC hypoxia-inducible factor 2 alpha (HIF2alpha). The antisense compound
CC comprises an antisense oligonucleotide that specifically hybridises with
CC the nucleic acid and inhibits the expression of HIF1alpha and/or
CC HIF2alpha. The antisense oligonucleotide is a chimeric oligonucleotide.
CC The antisense oligonucleotide comprises at least one modified
CC internucleoside linkage, preferably a phosphorothioate linkage. It also
CC comprises at least one modified sugar moiety, preferably a 2'-O-
CC methoxyethyl (2'-MOE) sugar moiety. The antisense oligonucleotide further
CC comprises at least one modified nucleobase, preferably a 5-
CC methylcytosine. The antisense oligonucleotides are useful for the
CC treatment of diseases such as hyperproliferative disorders, e.g. cancer,
CC preferably a cancer carrying a p53 mutation, or an angiogenic disorder
CC that affects the eye. The compound is also useful for treating tumours,
CC hyperplasias, pulmonary fibrosis, angiogenesis, psoriasis,
CC atherosclerosis and smooth muscle cell proliferation in the blood vessels
CC such as stenosis or restenosis following angioplasty. It is also useful
CC in drug discovery and target validation, and can be utilised for
CC diagnostics, therapeutics, prophylaxis and as research reagents and kits.
CC The present sequence represents an oligonucleotide used in the examples
CC of the present invention.
XX
SQ Sequence 20 BP; 5 A; 4 C; 6 G; 5 T; 0 U; 0 Other;

Query Match 95.0%; Score 19; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.4;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 CTCATGGTCACATGGATGA 20
|||||||||||||||||||
Db 1 CTCATGGTCACATGGATGA 19

RESULT 3
ADT78571
ID ADT78571 standard; DNA; 20 BP.
XX
AC ADT78571;
XX
DT 27-JAN-2005 (first entry)
XX
DE HIF1alpha cDNA, antisense oligonucleotide ISIS #298697.
XX
KW Antisense therapy; human; hypoxia-inducible factor 1 alpha;
KW hypoxia-inducible factor 2 alpha; HIF1alpha; HIF2alpha;
KW hyperproliferative disorder; cancer; p53; angiogenic disorder;

```
KW   eye disorder; tumour; hyperplasia; pulmonary fibrosis; angiogenesis;
KW   psoriasis; atherosclerosis; smooth muscle cell proliferation;
KW   blood vessel; restenosis; angioplasty; cytostatic; angiogenesis;
KW   ophthalmological; antiinflammatory; respiratory; vasotropic; mouse; rat;
KW   phosphorothioate; ss.
XX
OS   Homo sapiens.
OS   Mus musculus.
OS   Rattus sp.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1. .20
FT                   /*tag=  b
FT                   /mod_base= OTHER
FT                   /note= "Phosphorothioate backbone. All cytidines are 5-
FT                   methylcytidines"
FT   modified_base   1. .5
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "2'-O-Methoxyethyl (2'-MOE) nucleotides"
FT   modified_base   16. .20
FT                   /*tag=  c
FT                   /mod_base= OTHER
FT                   /note= "2'-O-Methoxyethyl (2'-MOE) nucleotides"
XX
PN   US2004220393-A1.
XX
PD   04-NOV-2004.
XX
PF   21-NOV-2003; 2003US-00719370.
XX
PR   23-NOV-2002; 2002US-00304126.
XX
PA   (WARD/) WARD D T.
PA   (DOBI/) DOBIE K W.
PA   (MARC/) MARCUSSON E G.
PA   (FREI/) FREIER S M.
XX
PI   Ward DT,  Dobie KW,  Marcusson EG,  Freier SM;
XX
DR   WPI; 2004-774955/76.
XX
PT   New antisense compound which inhibits the expression of hypoxia-inducible
PT   factor 1 alpha (HIF1 alpha) and/or HIF2 alpha, useful for treating
PT   hyperproliferative disorder, e.g. cancer carrying a p53 mutation.
XX
PS   Claim 27; SEQ ID NO 141; 195pp; English.
XX
CC   The present invention relates to antisense compounds targeted to nucleic
CC   acids encoding hypoxia-inducible factor 1 alpha (HIF1alpha) and/or
CC   hypoxia-inducible factor 2 alpha (HIF2alpha). The antisense compound
CC   comprises an antisense oligonucleotide that specifically hybridises with
CC   the nucleic acid and inhibits the expression of HIF1alpha and/or
CC   HIF2alpha. The antisense oligonucleotide is a chimeric oligonucleotide.
CC   The antisense oligonucleotide comprises at least one modified
CC   internucleoside linkage, preferably a phosphorothioate linkage. It also
CC   comprises at least one modified sugar moiety, preferably a 2'-O-
CC   methoxyethyl (2'-MOE) sugar moiety. The antisense oligonucleotide further
CC   comprises at least one modified nucleobase, preferably a 5-
CC   methylcytosine. The antisense oligonucleotides are useful for the
CC   treatment of diseases such as hyperproliferative disorders, e.g. cancer,
CC   preferably a cancer carrying a p53 mutation, or an angiogenic disorder
CC   that affects the eye. The compound is also useful for treating tumours,
CC   hyperplasias, pulmonary fibrosis, angiogenesis, psoriasis,
CC   atherosclerosis and smooth muscle cell proliferation in the blood vessels
CC   such as stenosis or restenosis following angioplasty. It is also useful
CC   in drug discovery and target validation, and can be utilised for
CC   diagnostics, therapeutics, prophylaxis and as research reagents and kits.
CC   The present sequence represents an antisense oligonucleotide used in the
CC   examples of the present invention.
XX
SQ   Sequence 20 BP; 4 A; 5 C; 5 G; 6 T; 0 U; 0 Other;

  Query Match            95.0%;  Score 19;  DB 1;  Length 20;
  Best Local Similarity  100.0%;  Pred. No. 2.4;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CCTCATGGTCACATGGATG 19
              |||||||||||||||||||
Db          2 CCTCATGGTCACATGGATG 20


RESULT 4
ADT78881
ID   ADT78881 standard; DNA; 20 BP.
XX
AC   ADT78881;
XX
DT   27-JAN-2005  (first entry)
XX
DE   Antisense oligonucleotide (ISIS 337224) for human HIF1alpha/HIF2alpha.
XX
KW   Antisense therapy; human; hypoxia-inducible factor 1 alpha;
KW   hypoxia-inducible factor 2 alpha; HIF1alpha; HIF2alpha;
KW   hyperproliferative disorder; cancer; p53; angiogenic disorder;
KW   eye disorder; tumour; hyperplasia; pulmonary fibrosis; angiogenesis;
KW   psoriasis; atherosclerosis; smooth muscle cell proliferation;
KW   blood vessel; restenosis; angioplasty; cytostatic; angiogenesis;
KW   ophthalmological; antiinflammatory; respiratory; vasotropic; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   modified_base   11
FT                   /*tag=  a
FT                   /mod_base= i
FT   modified_base   14
FT                   /*tag=  b
FT                   /mod_base= OTHER
FT                   /note= "OTHER= Pseudouridine"
XX
PN   US2004220393-A1.
XX
PD   04-NOV-2004.
XX
PF   21-NOV-2003; 2003US-00719370.
XX
PR   23-NOV-2002; 2002US-00304126.
XX
PA   (WARD/) WARD D T.
PA   (DOBI/) DOBIE K W.
PA   (MARC/) MARCUSSON E G.
PA   (FREI/) FREIER S M.
XX
PI   Ward DT,  Dobie KW,  Marcusson EG,  Freier SM;
XX
DR   WPI; 2004-774955/76.
XX
PT   New antisense compound which inhibits the expression of hypoxia-inducible
PT   factor 1 alpha (HIF1 alpha) and/or HIF2 alpha, useful for treating
PT   hyperproliferative disorder, e.g. cancer carrying a p53 mutation.
XX
PS   Example 30; SEQ ID NO 452; 195pp; English.
XX
CC   The present invention relates to antisense compounds targeted to nucleic
CC   acids encoding hypoxia-inducible factor 1 alpha (HIF1alpha) and/or
CC   hypoxia-inducible factor 2 alpha (HIF2alpha). The antisense compound
CC   comprises an antisense oligonucleotide that specifically hybridises with
CC   the nucleic acid and inhibits the expression of HIF1alpha and/or
CC   HIF2alpha. The antisense oligonucleotide is a chimeric oligonucleotide.
CC   The antisense oligonucleotide comprises at least one modified
CC   internucleoside linkage, preferably a phosphorothioate linkage. It also
CC   comprises at least one modified sugar moiety, preferably a 2'-O-
CC   methoxyethyl (2'-MOE) sugar moiety. The antisense oligonucleotide further
CC   comprises at least one modified nucleobase, preferably a 5-
CC   methylcytosine. The antisense oligonucleotides are useful for the
```

```
CC   treatment of diseases such as hyperproliferative disorders, e.g. cancer,
CC   preferably a cancer carrying a p53 mutation, or an angiogenic disorder
CC   that affects the eye. The compound is also useful for treating tumours,
CC   hyperplasias, pulmonary fibrosis, angiogenesis, psoriasis,
CC   atherosclerosis and smooth muscle cell proliferation in the blood vessels
CC   such as stenosis or restenosis following angioplasty. It is also useful
CC   in drug discovery and target validation, and can be utilised for
CC   diagnostics, therapeutics, prophylaxis and as research reagents and kits.
CC   The present sequence represents an oligonucleotide used in the examples
CC   of the present invention.
XX
SQ   Sequence 20 BP; 4 A; 5 C; 5 G; 4 T; 0 U; 2 Other;

  Query Match             90.0%;  Score 18;  DB 1;  Length 20;
  Best Local Similarity   90.0%;  Pred. No. 3.5;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 CCTCATGGTCACATGGATGA 20
              |||||||||| || ||||||
Db          1 CCTCATGGTCNCANGGATGA 20


RESULT 5
ADT78874
ID   ADT78874 standard; DNA; 20 BP.
XX
AC   ADT78874;
XX
DT   27-JAN-2005  (first entry)
XX
DE   Antisense oligonucleotide (ISIS 330447) for human HIF1alpha.
XX
KW   Antisense therapy; human; hypoxia-inducible factor 1 alpha;
KW   hypoxia-inducible factor 2 alpha; HIF1alpha; HIF2alpha;
KW   hyperproliferative disorder; cancer; p53; angiogenic disorder;
KW   eye disorder; tumour; hyperplasia; pulmonary fibrosis; angiogenesis;
KW   psoriasis; atherosclerosis; smooth muscle cell proliferation;
KW   blood vessel; restenosis; angioplasty; cytostatic; angiogenesis;
KW   ophthalmological; antiinflammatory; respiratory; vasotropic; ss.
XX
OS   Homo sapiens.
XX
PN   US2004220393-A1.
XX
PD   04-NOV-2004.
XX
PF   21-NOV-2003; 2003US-00719370.
XX
PR   23-NOV-2002; 2002US-00304126.
XX
PA   (WARD/) WARD D T.
PA   (DOBI/) DOBIE K W.
PA   (MARC/) MARCUSSON E G.
PA   (FREI/) FREIER S M.
XX
PI   Ward DT,  Dobie KW,  Marcusson EG,  Freier SM;
XX
DR   WPI; 2004-774955/76.
XX
PT   New antisense compound which inhibits the expression of hypoxia-inducible
PT   factor 1 alpha (HIF1 alpha) and/or HIF2 alpha, useful for treating
PT   hyperproliferative disorder, e.g. cancer carrying a p53 mutation.
XX
PS   Claim 92; SEQ ID NO 445; 195pp; English.
XX
CC   The present invention relates to antisense compounds targeted to nucleic
CC   acids encoding hypoxia-inducible factor 1 alpha (HIF1alpha) and/or
CC   hypoxia-inducible factor 2 alpha (HIF2alpha). The antisense compound
CC   comprises an antisense oligonucleotide that specifically hybridises with
CC   the nucleic acid and inhibits the expression of HIF1alpha and/or
CC   HIF2alpha. The antisense oligonucleotide is a chimeric oligonucleotide.
CC   The antisense oligonucleotide comprises at least one modified
CC   internucleoside linkage, preferably a phosphorothioate linkage. It also
CC   comprises at least one modified sugar moiety, preferably a 2'-O-
CC   methoxyethyl (2'-MOE) sugar moiety. The antisense oligonucleotide further
CC   comprises at least one modified nucleobase, preferably a 5-
CC   methylcytosine. The antisense oligonucleotides are useful for the
CC   treatment of diseases such as hyperproliferative disorders, e.g. cancer,
CC   preferably a cancer carrying a p53 mutation, or an angiogenic disorder
CC   that affects the eye. The compound is also useful for treating tumours,
CC   hyperplasias, pulmonary fibrosis, angiogenesis, psoriasis,
CC   atherosclerosis and smooth muscle cell proliferation in the blood vessels
CC   such as stenosis or restenosis following angioplasty. It is also useful
CC   in drug discovery and target validation, and can be utilised for
CC   diagnostics, therapeutics, prophylaxis and as research reagents and kits.
CC   The present sequence represents an oligonucleotide used in the examples
CC   of the present invention.
XX
SQ   Sequence 20 BP; 5 A; 3 C; 6 G; 6 T; 0 U; 0 Other;

  Query Match             90.0%;  Score 18;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 3.5;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 TCATGGTCACATGGATGA 20
              ||||||||||||||||||
Db          1 TCATGGTCACATGGATGA 18


RESULT 6
ADQ88746
ID   ADQ88746 standard; DNA; 20 BP.
XX
AC   ADQ88746;
XX
DT   21-OCT-2004  (first entry)
XX
DE   Human HIF-1 antisense oligonucleotide RX-0041.
XX
KW   RX-0047; RX-0149; human; hypoxia inducible factor; HIF-1; cytotoxicity;
KW   cancer; infection; inflammation; tumour formation; ss;
KW   antisense oligonucleotide; antisense technology; RX-0158; RX-0041.
XX
OS   Homo sapiens.
XX
PN   US2004152655-A1.
XX
PD   05-AUG-2004.
XX
PF   28-JAN-2004; 2004US-00766185.
XX
PR   31-JAN-2003; 2003US-0444367P.
XX
PA   (YOON/) YOON H.
PA   (MAOL/) MAO L.
PA   (LEEY/) LEE Y B.
PA   (AHNC/) AHN C.
PA   (JIAN/) JIANG X.
XX
PI   Yoon H,  Mao L,  Lee YB,  Ahn C,  Jiang X;
XX
DR   WPI; 2004-561492/54.
XX
PT   New RX-0047 and RX-0149 antisense oligonucleotide compounds targeted to a
PT   nucleic acid molecule encoding human hypoxia inducible factor (HIF-1),
PT   useful for inhibiting expression of HIF-1 and inducing cytotoxicity in
PT   several cancer cells.
XX
PS   Example 4; SEQ ID NO 26; 35pp; English.
XX
CC   The invention describes a compound, RX-0047 or RX-0149 targeted to a
CC   nucleic acid molecule encoding human hypoxia inducible factor (HIF-1),
CC   where the oligonucleotide compound inhibits the expression of human HIF-
CC   1. Also described are: a method of inhibiting the expression HIF-1 in
CC   human cells or tissues; and a method of inducing cytotoxicity in a cancer
CC   cell. Specifically claimed are RX-0047 and RX-0149 compounds having a
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CC   fully defined sequence comprising 20 bp (SEQ ID NO. 2, 5'
CC   aatgagccaccagtgtccaa 3' and SEQ ID NO. 4, 5' ggagctaacatctccaagtc 3',
CC   respectively). The compounds are useful for inhibiting the expression of
CC   HIF-1 and inducing the cytotoxicity in several cancer cells. The
CC   antisense compounds are also useful for preventing or delaying infection,
CC   inflammation, or tumour formation. This sequence represents a human HIF-1
CC   antisense oligonucleotide.
XX
SQ   Sequence 20 BP; 6 A; 3 C; 6 G; 5 T; 0 U; 0 Other;

  Query Match             85.0%;  Score 17;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 5.1;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 CATGGTCACATGGATGA 20
              |||||||||||||||||
Db          1 CATGGTCACATGGATGA 17


RESULT 7
ADT78880
ID   ADT78880 standard; DNA; 20 BP.
XX
AC   ADT78880;
XX
DT   27-JAN-2005  (first entry)
XX
DE   Antisense oligonucleotide (ISIS 337223) for human HIF1alpha/HIF2alpha.
XX
KW   Antisense therapy; human; hypoxia-inducible factor 1 alpha;
KW   hypoxia-inducible factor 2 alpha; HIF1alpha; HIF2alpha;
KW   hyperproliferative disorder; cancer; p53; angiogenic disorder;
KW   eye disorder; tumour; hyperplasia; pulmonary fibrosis; angiogenesis;
KW   psoriasis; atherosclerosis; smooth muscle cell proliferation;
KW   blood vessel; restenosis; angioplasty; cytostatic; angiogenesis;
KW   ophthalmological; antiinflammatory; respiratory; vasotropic; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   modified_base   12
FT                   /*tag=  a
FT                   /mod_base= i
FT   modified_base   15
FT                   /*tag=  b
FT                   /mod_base= OTHER
FT                   /note= "OTHER= Pseudouridine"
XX
PN   US2004220393-A1.
XX
PD   04-NOV-2004.
XX
PF   21-NOV-2003; 2003US-00719370.
XX
PR   23-NOV-2002; 2002US-00304126.
XX
PA   (WARD/) WARD D T.
PA   (DOBI/) DOBIE K W.
PA   (MARC/) MARCUSSON E G.
PA   (FREI/) FREIER S M.
XX
PI   Ward DT,  Dobie KW,  Marcusson EG,  Freier SM;
XX
DR   WPI; 2004-774955/76.
XX
PT   New antisense compound which inhibits the expression of hypoxia-inducible
PT   factor 1 alpha (HIF1 alpha) and/or HIF2 alpha, useful for treating
PT   hyperproliferative disorder, e.g. cancer carrying a p53 mutation.
XX
PS   Example 30; SEQ ID NO 451; 195pp; English.
XX
CC   The present invention relates to antisense compounds targeted to nucleic
CC   acids encoding hypoxia-inducible factor 1 alpha (HIF1alpha) and/or
CC   hypoxia-inducible factor 2 alpha (HIF2alpha). The antisense compound
CC   comprises an antisense oligonucleotide that specifically hybridises with
CC   the nucleic acid and inhibits the expression of HIF1alpha and/or
CC   HIF2alpha. The antisense oligonucleotide is a chimeric oligonucleotide.
CC   The antisense oligonucleotide comprises at least one modified
CC   internucleoside linkage, preferably a phosphorothioate linkage. It also
CC   comprises at least one modified sugar moiety, preferably a 2'-O-
CC   methoxyethyl (2'-MOE) sugar moiety. The antisense oligonucleotide further
CC   comprises at least one modified nucleobase, preferably a 5-
CC   methylcytosine. The antisense oligonucleotides are useful for the
CC   treatment of diseases such as hyperproliferative disorders, e.g. cancer,
CC   preferably a cancer carrying a p53 mutation, or an angiogenic disorder
CC   that affects the eye. The compound is also useful for treating tumours,
CC   hyperplasias, pulmonary fibrosis, angiogenesis, psoriasis,
CC   atherosclerosis and smooth muscle cell proliferation in the blood vessels
CC   such as stenosis or restenosis following angioplasty. It is also useful
CC   in drug discovery and target validation, and can be utilised for
CC   diagnostics, therapeutics, prophylaxis and as research reagents and kits.
CC   The present sequence represents an oligonucleotide used in the examples
CC   of the present invention.
XX
SQ   Sequence 20 BP; 3 A; 5 C; 5 G; 5 T; 0 U; 2 Other;

  Query Match             85.0%;  Score 17;  DB 1;  Length 20;
  Best Local Similarity   89.5%;  Pred. No. 5.1;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 CCTCATGGTCACATGGATG 19
              |||||||||| || |||||
Db          2 CCTCATGGTCNCANGGATG 20


RESULT 8
ADT78872
ID   ADT78872 standard; DNA; 20 BP.
XX
AC   ADT78872;
XX
DT   27-JAN-2005  (first entry)
XX
DE   Antisense oligonucleotide (ISIS 330460) for human HIF2alpha.
XX
KW   Antisense therapy; human; hypoxia-inducible factor 1 alpha;
KW   hypoxia-inducible factor 2 alpha; HIF1alpha; HIF2alpha;
KW   hyperproliferative disorder; cancer; p53; angiogenic disorder;
KW   eye disorder; tumour; hyperplasia; pulmonary fibrosis; angiogenesis;
KW   psoriasis; atherosclerosis; smooth muscle cell proliferation;
KW   blood vessel; restenosis; angioplasty; cytostatic; angiogenesis;
KW   ophthalmological; antiinflammatory; respiratory; vasotropic; ss.
XX
OS   Homo sapiens.
XX
PN   US2004220393-A1.
XX
PD   04-NOV-2004.
XX
PF   21-NOV-2003; 2003US-00719370.
XX
PR   23-NOV-2002; 2002US-00304126.
XX
PA   (WARD/) WARD D T.
PA   (DOBI/) DOBIE K W.
PA   (MARC/) MARCUSSON E G.
PA   (FREI/) FREIER S M.
XX
PI   Ward DT,  Dobie KW,  Marcusson EG,  Freier SM;
XX
DR   WPI; 2004-774955/76.
XX
PT   New antisense compound which inhibits the expression of hypoxia-inducible
PT   factor 1 alpha (HIF1 alpha) and/or HIF2 alpha, useful for treating
PT   hyperproliferative disorder, e.g. cancer carrying a p53 mutation.
XX
```

```
PS   Claim 92; SEQ ID NO 443; 195pp; English.
XX
CC   The present invention relates to antisense compounds targeted to nucleic
CC   acids encoding hypoxia-inducible factor 1 alpha (HIF1alpha) and/or
CC   hypoxia-inducible factor 2 alpha (HIF2alpha). The antisense compound
CC   comprises an antisense oligonucleotide that specifically hybridises with
CC   the nucleic acid and inhibits the expression of HIF1alpha and/or
CC   HIF2alpha. The antisense oligonucleotide is a chimeric oligonucleotide.
CC   The antisense oligonucleotide comprises at least one modified
CC   internucleoside linkage, preferably a phosphorothioate linkage. It also
CC   comprises at least one modified sugar moiety, preferably a 2'-O-
CC   methoxyethyl (2'-MOE) sugar moiety. The antisense oligonucleotide further
CC   comprises at least one modified nucleobase, preferably a 5-
CC   methylcytosine. The antisense oligonucleotides are useful for the
CC   treatment of diseases such as hyperproliferative disorders, e.g. cancer,
CC   preferably a cancer carrying a p53 mutation, or an angiogenic disorder
CC   that affects the eye. The compound is also useful for treating tumours,
CC   hyperplasias, pulmonary fibrosis, angiogenesis, psoriasis,
CC   atherosclerosis and smooth muscle cell proliferation in the blood vessels
CC   such as stenosis or restenosis following angioplasty. It is also useful
CC   in drug discovery and target validation, and can be utilised for
CC   diagnostics, therapeutics, prophylaxis and as research reagents and kits.
CC   The present sequence represents an oligonucleotide used in the examples
CC   of the present invention.
XX
SQ   Sequence 20 BP; 4 A; 5 C; 7 G; 4 T; 0 U; 0 Other;

  Query Match             84.0%;  Score 16.8;  DB 1;  Length 20;
  Best Local Similarity   90.0%;  Pred. No. 5.5;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 CCTCATGGTCACATGGATGA 20
              |||||||||| || ||||||
Db          1 CCTCATGGTCGCAGGGATGA 20


RESULT 9
ADT78877
ID   ADT78877 standard; DNA; 20 BP.
XX
AC   ADT78877;
XX
DT   27-JAN-2005  (first entry)
XX
DE   Antisense oligonucleotide (ISIS 330452) for human HIF1alpha.
XX
KW   Antisense therapy; human; hypoxia-inducible factor 1 alpha;
KW   hypoxia-inducible factor 2 alpha; HIF1alpha; HIF2alpha;
KW   hyperproliferative disorder; cancer; p53; angiogenic disorder;
KW   eye disorder; tumour; hyperplasia; pulmonary fibrosis; angiogenesis;
KW   psoriasis; atherosclerosis; smooth muscle cell proliferation;
KW   blood vessel; restenosis; angioplasty; cytostatic; angiogenesis;
KW   ophthalmological; antiinflammatory; respiratory; vasotropic; ss.
XX
OS   Homo sapiens.
XX
PN   US2004220393-A1.
XX
PD   04-NOV-2004.
XX
PF   21-NOV-2003; 2003US-00719370.
XX
PR   23-NOV-2002; 2002US-00304126.
XX
PA   (WARD/) WARD D T.
PA   (DOBI/) DOBIE K W.
PA   (MARC/) MARCUSSON E G.
PA   (FREI/) FREIER S M.
XX
PI   Ward DT,  Dobie KW,  Marcusson EG,  Freier SM;
XX
DR   WPI; 2004-774955/76.
XX
PT   New antisense compound which inhibits the expression of hypoxia-inducible
PT   factor 1 alpha (HIF1 alpha) and/or HIF2 alpha, useful for treating
PT   hyperproliferative disorder, e.g. cancer carrying a p53 mutation.
XX
PS   Claim 92; SEQ ID NO 448; 195pp; English.
XX
CC   The present invention relates to antisense compounds targeted to nucleic
CC   acids encoding hypoxia-inducible factor 1 alpha (HIF1alpha) and/or
CC   hypoxia-inducible factor 2 alpha (HIF2alpha). The antisense compound
CC   comprises an antisense oligonucleotide that specifically hybridises with
CC   the nucleic acid and inhibits the expression of HIF1alpha and/or
CC   HIF2alpha. The antisense oligonucleotide is a chimeric oligonucleotide.
CC   The antisense oligonucleotide comprises at least one modified
CC   internucleoside linkage, preferably a phosphorothioate linkage. It also
CC   comprises at least one modified sugar moiety, preferably a 2'-O-
CC   methoxyethyl (2'-MOE) sugar moiety. The antisense oligonucleotide further
CC   comprises at least one modified nucleobase, preferably a 5-
CC   methylcytosine. The antisense oligonucleotides are useful for the
CC   treatment of diseases such as hyperproliferative disorders, e.g. cancer,
CC   preferably a cancer carrying a p53 mutation, or an angiogenic disorder
CC   that affects the eye. The compound is also useful for treating tumours,
CC   hyperplasias, pulmonary fibrosis, angiogenesis, psoriasis,
CC   atherosclerosis and smooth muscle cell proliferation in the blood vessels
CC   such as stenosis or restenosis following angioplasty. It is also useful
CC   in drug discovery and target validation, and can be utilised for
CC   diagnostics, therapeutics, prophylaxis and as research reagents and kits.
CC   The present sequence represents an oligonucleotide used in the examples
CC   of the present invention.
XX
SQ   Sequence 20 BP; 4 A; 5 C; 4 G; 7 T; 0 U; 0 Other;

  Query Match             80.0%;  Score 16;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 7.3;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CCTCATGGTCACATGG 16
              ||||||||||||||||
Db          5 CCTCATGGTCACATGG 20


RESULT 10
ADT78879
ID   ADT78879 standard; DNA; 20 BP.
XX
AC   ADT78879;
XX
DT   27-JAN-2005  (first entry)
XX
DE   Antisense oligonucleotide (ISIS 326743) for human HIF2alpha.
XX
KW   Antisense therapy; human; hypoxia-inducible factor 1 alpha;
KW   hypoxia-inducible factor 2 alpha; HIF1alpha; HIF2alpha;
KW   hyperproliferative disorder; cancer; p53; angiogenic disorder;
KW   eye disorder; tumour; hyperplasia; pulmonary fibrosis; angiogenesis;
KW   psoriasis; atherosclerosis; smooth muscle cell proliferation;
KW   blood vessel; restenosis; angioplasty; cytostatic; angiogenesis;
KW   ophthalmological; antiinflammatory; respiratory; vasotropic; ss.
XX
OS   Homo sapiens.
XX
PN   US2004220393-A1.
XX
PD   04-NOV-2004.
XX
PF   21-NOV-2003; 2003US-00719370.
XX
PR   23-NOV-2002; 2002US-00304126.
XX
PA   (WARD/) WARD D T.
PA   (DOBI/) DOBIE K W.
PA   (MARC/) MARCUSSON E G.
PA   (FREI/) FREIER S M.
XX
```

PI Ward DT, Dobie KW, Marcusson EG, Freier SM;
XX
DR WPI; 2004-774955/76.
XX
PT New antisense compound which inhibits the expression of hypoxia-inducible
PT factor 1 alpha (HIF1 alpha) and/or HIF2 alpha, useful for treating
PT hyperproliferative disorder, e.g. cancer carrying a p53 mutation.
XX
PS Claim 92; SEQ ID NO 450; 195pp; English.
XX
CC The present invention relates to antisense compounds targeted to nucleic
CC acids encoding hypoxia-inducible factor 1 alpha (HIF1alpha) and/or
CC hypoxia-inducible factor 2 alpha (HIF2alpha). The antisense compound
CC comprises an antisense oligonucleotide that specifically hybridises with
CC the nucleic acid and inhibits the expression of HIF1alpha and/or
CC HIF2alpha. The antisense oligonucleotide is a chimeric oligonucleotide.
CC The antisense oligonucleotide comprises at least one modified
CC internucleoside linkage, preferably a phosphorothioate linkage. It also
CC comprises at least one modified sugar moiety, preferably a 2'-O-
CC methoxyethyl (2'-MOE) sugar moiety. The antisense oligonucleotide further
CC comprises at least one modified nucleobase, preferably a 5-
CC methylcytosine. The antisense oligonucleotides are useful for the
CC treatment of diseases such as hyperproliferative disorders, e.g. cancer,
CC preferably a cancer carrying a p53 mutation, or an angiogenic disorder
CC that affects the eye. The compound is also useful for treating tumours,
CC hyperplasias, pulmonary fibrosis, angiogenesis, psoriasis,
CC atherosclerosis and smooth muscle cell proliferation in the blood vessels
CC such as stenosis or restenosis following angioplasty. It is also useful
CC in drug discovery and target validation, and can be utilised for
CC diagnostics, therapeutics, prophylaxis and as research reagents and kits.
CC The present sequence represents an oligonucleotide used in the examples
CC of the present invention.
XX
SQ Sequence 20 BP; 3 A; 5 C; 7 G; 5 T; 0 U; 0 Other;

Query Match 79.0%; Score 15.8; DB 1; Length 20;
Best Local Similarity 89.5%; Pred. No. 7.9;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCTCATGGTCACATGGATG 19
||||||||| || |||||
Db 2 CCTCATGGTCGCAGGGATG 20

RESULT 11
AAV13322
ID AAV13322 standard; DNA; 19 BP.
XX
AC AAV13322;
XX
DT 14-MAY-1998 (first entry)
XX
DE Sense primer Exon 4 for human 5-lipoxygenase gene.
XX
KW Inflammatory disease; polymorphism; 5-lipoxygenase; asthma;
KW ulcerative colitis; bronchitis; sinusitis; psoriasis; rhinitis;
KW arthritis; diagnosis; treatment; PCR primer; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO9742347-A2.
XX
PD 13-NOV-1997.
XX
PF 29-APR-1997; 97WO-US007137.
XX
PR 06-MAY-1996; 96US-0016890P.
PR 25-APR-1997; 97US-00846020.
XX
PA (BGHM) BRIGHAM & WOMENS HOSPITAL.
XX
PI Drazen JM, In K, Asano K, Beier D, Grobholz J;
XX
DR WPI; 1997-558997/51.
XX
PT Classifying patients with inflammatory disease, specifically asthma -
PT according to polymorphisms in 5-lipoxygenase gene regulatory region, e.g.
PT to identify candidates for lipoxygenase inhibitor treatment.
XX
PS Example 1; Page 19; 56pp; English.
XX
CC The present sequence was used in the development of a novel method for
CC classifying patients suffering from an inflammatory disease. The method
CC comprises identifying in DNA from at least 1 patient a sequence
CC polymorphism, as compared with the normal 5-lipoxygenase (5-LOX) gene
CC (AAT88431), in a 5-LOX regulatory gene sequence. The method can be
CC applied to subjects with asthma, ulcerative colitis, bronchitis,
CC sinusitis, psoriasis, allergic and non-allergic rhinitis, lupus or
CC rheumatoid arthritis. Specifically it can be used to diagnose asthma or
CC susceptibility to disease, identify treatments suitable for individual
CC patients or assess the likely success of treatment
XX
SQ Sequence 19 BP; 4 A; 4 C; 5 G; 6 T; 0 U; 0 Other;

Query Match 74.0%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred. No. 10;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CTCATGGTCACATGGATG 19
|||||| ||| |||||||
Db 2 CTCATGCTCAGATGGATG 19

RESULT 12
ADZ58131
ID ADZ58131 standard; RNA; 19 BP.
XX
AC ADZ58131;
XX
DT 30-JUN-2005 (first entry)
XX
DE Antisense siRNA oligo that modulates human HIF1 expression Seq 259.
XX
KW ss; short interfering RNA; siRNA; gene silencing; RNA interference;
KW hypoxia inducible factor 1; cancer; hyperproliferation;
KW macular degeneration; diabetic retinopathy; cytostatic; ophthalmological;
KW antidiabetic; antisense.
XX
OS Homo sapiens.
XX
PN WO2005035759-A2.
XX
PD 21-APR-2005.
XX
PF 20-AUG-2004; 2004WO-US027294.
XX
PR 20-AUG-2003; 2003US-0496655P.
PR 23-OCT-2003; 2003US-00693059.
PR 24-NOV-2003; 2003US-00720448.
PR 03-DEC-2003; 2003US-00727780.
PR 14-JAN-2004; 2004US-00757803.
PR 10-FEB-2004; 2004US-0543480P.
PR 13-FEB-2004; 2004US-00780447.
PR 16-APR-2004; 2004US-00826966.
PR 30-APR-2004; 54US-09997777.
PR 24-MAY-2004; 54US-09996666.
XX
PA (SIRN-) SIRNA THERAPEUTICS INC.
XX
PI Usman N, Mcswiggen J;
XX
DR WPI; 2005-306364/31.
XX
PT New chemically synthesized double stranded short interfering nucleic acid
PT molecule that directs cleavage of a hypoxia inducible factor 1 RNA via

PT RNA interference (RNAi), useful for modulating HIF1, its expression or
PT activity.
XX
PS Claim 33; SEQ ID NO 259; 189pp; English.
XX
CC This invention relates to a novel chemically synthesized double stranded
CC short interfering nucleic acid strand (siNA). Specifically, it refers to
CC siNAs that direct cleavage of a hypoxia inducible factor 1 (HIF1) RNA via
CC RNA interference (RNAi). In particular, the siNAs may include short
CC interfering RNA (siRNA), double-stranded RNA (dsRNA), micro-RNA (miRNA)
CC and short hairpin RNA (shRNA) molecules that are capable of mediating
CC RNAi. The present invention describes a sense strand of a double-stranded
CC siNA that comprises a nucleotide sequence that is complementary to HIF1
CC RNA or a portion thereof, and where a second strand is the complementary
CC antisense siNA strand. Note that the sense region is connected to the
CC antisense region via a polynucleotide linker molecule. Accordingly, these
CC siNAs are useful in providing compositions for the treatment of traits,
CC diseases and conditions that respond to modulation of HIF1 expression,
CC namely cancer and proliferative conditions including macular
CC degeneration, diabetic retinopathy and other conditions associated with
CC hypoxia inducible proliferation. As such, these compositions exhibit
CC cytostatic, ophthalmological and antidiabetic activities. This
CC oligonucleotide sequence is an antisense siRNA strand that targets human
CC HIF1 RNA to modulate expression given in an exemplification of the
CC invention.
XX
SQ Sequence 19 BP; 7 A; 2 C; 6 G; 0 T; 4 U; 0 Other;

```
  Query Match             70.0%;  Score 14;  DB 1;  Length 19;
  Best Local Similarity   78.6%;  Pred. No. 13;
  Matches   11;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 GGTCACATGGATGA 20
              ||:||||:|||:||
Db          1 GGUCACAUGGAUGA 14
```

RESULT 13
ADZ57911/c
ID ADZ57911 standard; RNA; 19 BP.
XX
AC ADZ57911;
XX
DT 30-JUN-2005 (first entry)
XX
DE Sense siRNA oligo that modulates human HIF1 expression Seq 39.
XX
KW ss; short interfering RNA; siRNA; gene silencing; RNA interference;
KW hypoxia inducible factor 1; cancer; hyperproliferation;
KW macular degeneration; diabetic retinopathy; cytostatic; ophthalmological;
KW antidiabetic.
XX
OS Homo sapiens.
XX
PN WO2005035759-A2.
XX
PD 21-APR-2005.
XX
PF 20-AUG-2004; 2004WO-US027294.
XX
PR 20-AUG-2003; 2003US-0496655P.
PR 23-OCT-2003; 2003US-00693059.
PR 24-NOV-2003; 2003US-00720448.
PR 03-DEC-2003; 2003US-00727780.
PR 14-JAN-2004; 2004US-00757803.
PR 10-FEB-2004; 2004US-0543480P.
PR 13-FEB-2004; 2004US-00780447.
PR 16-APR-2004; 2004US-00826966.
PR 30-APR-2004; 54US-09997777.
PR 24-MAY-2004; 54US-09996666.
XX
PA (SIRN-) SIRNA THERAPEUTICS INC.
XX
PI Usman N, Mcswiggen J;
XX
DR WPI; 2005-306364/31.
XX
PT New chemically synthesized double stranded short interfering nucleic acid
PT molecule that directs cleavage of a hypoxia inducible factor 1 RNA via
PT RNA interference (RNAi), useful for modulating HIF1, its expression or
PT activity.
XX
PS Claim 33; SEQ ID NO 39; 189pp; English.
XX
CC This invention relates to a novel chemically synthesized double stranded
CC short interfering nucleic acid strand (siNA). Specifically, it refers to
CC siNAs that direct cleavage of a hypoxia inducible factor 1 (HIF1) RNA via
CC RNA interference (RNAi). In particular, the siNAs may include short
CC interfering RNA (siRNA), double-stranded RNA (dsRNA), micro-RNA (miRNA)
CC and short hairpin RNA (shRNA) molecules that are capable of mediating
CC RNAi. The present invention describes a sense strand of a double-stranded
CC siNA that comprises a nucleotide sequence that is complementary to HIF1
CC RNA or a portion thereof, and where a second strand is the complementary
CC antisense siNA strand. Note that the sense region is connected to the
CC antisense region via a polynucleotide linker molecule. Accordingly, these
CC siNAs are useful in providing compositions for the treatment of traits,
CC diseases and conditions that respond to modulation of HIF1 expression,
CC namely cancer and proliferative conditions including macular
CC degeneration, diabetic retinopathy and other conditions associated with
CC hypoxia inducible proliferation. As such, these compositions exhibit
CC cytostatic, ophthalmological and antidiabetic activities. This
CC oligonucleotide sequence is a sense siRNA strand that targets human HIF1
CC RNA to modulate expression given in an exemplification of the invention.
XX
SQ Sequence 19 BP; 4 A; 6 C; 2 G; 0 T; 7 U; 0 Other;

```
  Query Match             70.0%;  Score 14;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 13;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 GGTCACATGGATGA 20
              ||||||||||||||
Db         19 GGTCACATGGATGA 6
```

RESULT 14
ABT38435/c
ID ABT38435 standard; DNA; 17 BP.
XX
AC ABT38435;
XX
DT 12-JUN-2003 (first entry)
XX
DE Tumour suppression related human fukutin oligo SEQ ID No 4072.
XX
KW Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; gene chip;
KW antisense; sense; tumour; cell degeneration; cancer; Alzheimer's disease;
KW schizophrenia; protein chip; gene therapy; tumour suppression;
KW human fukutin; ds.
XX
OS Homo sapiens.
XX
PN WO2003025175-A2.
XX
PD 27-MAR-2003.
XX
PF 17-SEP-2002; 2002WO-IB004208.
XX
PR 17-SEP-2001; 2001FR-00011978.
XX
PA (MOLE-) MOLECULAR ENGINES LAB.
XX
PI Telerman A, Amson R, Tuijnder M;
XX
DR WPI; 2003-313353/30.
XX

PT New isolated nucleic acid, useful for treating viral diseases associated
PT with tumors and cell degeneration, also related polypeptides, antibodies
PT and transfected cells.
XX
PS Disclosure; Page 510; 720pp; French.
XX
CC The invention relates to a novel isolated 17 mer nucleic acid sequence,
CC given in the specification, a sequence containing at least 15 consecutive
CC nucleotides from the 17 mer sequence, a sequence with, after optimal
CC alignment, at least 80 % identity to the 17 mer sequence, a sequence that
CC hybridizes to them under highly stringent conditions, or the complement
CC of any of them, or the corresponding RNA. The novel isolated nucleic
CC acids of the invention are useful as probes and primers for detecting,
CC identifying, quantifying and/or amplifying a nucleic acid, e.g. as one
CC component of a gene chip, in vitro as (anti)sense reagents, and for
CC production of recombinant polypeptides. Any of the nucleic acids,
CC polypeptides, vectors containing the nucleic acids, cells containing the
CC vector or antibodies directed against the polypeptides are useful for
CC preparation of pharmaceuticals for prevention and/or treatment of viral
CC diseases that are characterised by development of tumours or cell
CC degeneration, specifically cancer but also Alzheimer's disease and
CC schizophrenia. Analysis of the expression of the 17 mer nucleic acids in
CC patient samples is useful for diagnosis and/or prognosis of these
CC diseases. The polypeptides can also be used to generate antibodies, and
CC both the polypeptide and antibodies are useful as components of protein
CC chips. The nucleic acid sequences of the invention can be used in gene
CC therapy. This polynucleotide sequence represents a tumour suppression
CC related human fukutin oligonucleotide of the invention
XX
SQ Sequence 17 BP; 4 A; 4 C; 3 G; 6 T; 0 U; 0 Other;

Query Match 64.0%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 16;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 TCATGGTCACATGGAT 18
||| ||||| ||||||
Db 17 TCAAGGTCAAATGGAT 2

RESULT 15
ADW14071/c
ID ADW14071 standard; DNA; 18 BP.
XX
AC ADW14071;
XX
DT 07-APR-2005 (first entry)
XX
DE KCNMA1 exon 1B sense PCR primer, SEQ ID 3.
XX
KW Nootropic; autism; potassium channel; KCNMA1; PCR; primer; ss.
XX
OS Homo sapiens.
XX
PN FR2857452-A1.
XX
PD 14-JAN-2005.
XX
PF 11-JUL-2003; 2003FR-00008527.
XX
PR 11-JUL-2003; 2003FR-00008527.
XX
PA (UYRA-) UNIV RABELAIS FRANCOIS.
XX
PI Briault S, Laumonnier F, Le Guennec JY, Roger S;
XX
DR WPI; 2005-114499/13.
XX
PT Test for identifying autism, comprises detecting reduction in activity of
PT calcium-dependent potassium channels by measuring the electrical activity
PT of the channels.
XX
PS Example 1; SEQ ID NO 3; 42pp; French.
XX
CC The present invention relates to a test for detecting autism, which
CC comprises measuring the electrical activity of calcium-dependent
CC potassium channels (BKCa) in a sample of blood cells and detecting any
CC reduction in activity, relative to a control sample. Also claimed are:
CC selecting a subpopulation of patients with autism by performing the new
CC method and selecting subjects with reduced BKCa activity; and use of
CC activators or agonists of BKCa to prepare a composition for treating
CC autism where this is associated with deficient electrical activity. The
CC method is useful for autism diagnosis and prognosis and to identify a
CC subset of autism patients who may benefit from treatment with activators
CC or agonists (X) of BKCa, i.e. patients where autism is linked to a
CC defective electrical activity. In an example from the invention, a
CC translocation in the potassium channel KCNMA1 gene in a six year old
CC patient with autism was detected and characterized using PCR primers
CC ADW14069-ADW14128. The KCNMA1 gene encodes a protein of the glutaminergic
CC complex, and mutation of the KCNMA1 gene resulting in inadequate
CC functioning of BKCa. The translocation was [46, XY, t(9;10) (q23;q22)],
CC and the break was between the first and second exons of the KCNMA1 gene
CC and amplification tests showed that, in the patient, one copy of the
CC KCNMA1 was inactivated.
XX
SQ Sequence 18 BP; 4 A; 6 C; 5 G; 3 T; 0 U; 0 Other;

Query Match 64.0%; Score 12.8; DB 1; Length 18;
Best Local Similarity 87.5%; Pred. No. 18;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 CATGGTCACATGGATG 19
||||||||| |||||
Db 16 CATGGTCACCGGGATG 1

RESULT 16
ABN07620/c
ID ABN07620 standard; DNA; 17 BP.
XX
AC ABN07620;
XX
DT 29-MAY-2002 (first entry)
XX
DE Human GDMLP-1 17-mer scanning SEQ ID NO:5 sequence SEQ ID NO:7612.
XX
KW Human; genome-derived myosin-like protein 1; GDMLP-1; hGDMLP-1; heart;
KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;
KW skeletal muscle disorder; amplicon; screening; ss.
XX
OS Homo sapiens.
XX
PN WO200192524-A2.
XX
PD 06-DEC-2001.
XX
PF 25-MAY-2001; 2001WO-US016981.
XX
PR 26-MAY-2000; 2000US-0207456P.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
PR 30-JAN-2001; 2001WO-US000661.
PR 30-JAN-2001; 2001WO-US000662.
PR 30-JAN-2001; 2001WO-US000663.
PR 30-JAN-2001; 2001WO-US000664.
PR 30-JAN-2001; 2001WO-US000665.
PR 30-JAN-2001; 2001WO-US000666.
PR 30-JAN-2001; 2001WO-US000667.
PR 30-JAN-2001; 2001WO-US000668.
PR 30-JAN-2001; 2001WO-US000669.
PR 30-JAN-2001; 2001WO-US000670.
PR 05-FEB-2001; 2001US-0266860P.
XX
PA (AEOM-) AEOMICA INC.
XX

PI Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;
XX
DR WPI; 2002-179446/23.
XX
PT New polypeptide, for raising antibodies that recognize hGDMLP-1 proteins,
PT or as specific biomolecule capture probes for surface-enhanced laser
PT desorption ionization, comprises human myosin-like protein hGDMLP-1.
XX
PS Disclosure; SEQ ID NO 7612; 214pp; English.
XX
CC The present invention describes a human genome-derived myosin-like
CC protein 1 (hGDMLP-1). The protein and polynucleotide sequences of hGDMLP-
CC 1 can be used in gene therapy and vaccine production. The hGDMLP-1
CC nucleic acids can be used as probes to detect, characterise and quantify
CC hGDMLP-1 nucleic acids in samples, as amplification substrates, to
CC provide initial substrates for the recombinant engineering of hGDMLP-1
CC protein variants having desired phenotypic improvements, and for
CC expressing the proteins. The hGDMLP-1 proteins or polypeptides may be
CC used as immunogens to raise antibodies that specifically recognise hGDMLP
CC -1 proteins, as standards in assays used to determine the concentration
CC and/or amount specifically of hGDMLP proteins, as specific biomolecule
CC capture probes for surface-enhanced laser desorption ionisation, as
CC therapeutic supplement in patients having specific deficiency in hGDMLP-1
CC production, and in vaccines or for replacement therapy. The
CC polynucleotide sequences encoding hGDMLP-1 may be used for diagnosing a
CC disorder associated with the expression of hGDMLP-1, in particular heart
CC and skeletal muscle disorders. hGDMLP-1 is localised to chromosome 22.
CC The present sequence represents an oligomer used in the screening of the
CC hGDMLP-1 sequence in the exemplification of the present invention. N.B.
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequence
XX
SQ Sequence 17 BP; 3 A; 4 C; 5 G; 5 T; 0 U; 0 Other;

Query Match 61.0%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 20;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CCTCATGGTCACATGGA 17
||||| ||||||| | |
Db 17 CCTCAAGGTCACAGGTA 1

RESULT 17
ACN12001
ID ACN12001 standard; RNA; 17 BP.
XX
AC ACN12001;
XX
DT 22-APR-2004 (first entry)
XX
DE WNV minus strand Inozyme substrate SEQ ID NO 12004.
XX
KW WNV; West Nile Virus; antiinflammatory; cytostatic; hepatotropic;
KW virucide; neuroprotective; antibacterial; replication; pancreatitis;
KW encephalitis; myocarditis; meningitis; infection; hepatitis;
KW liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNAzyme;
KW Amberzyme; Zinzyme; ss.
XX
OS West Nile Virus.
XX
PN WO200268637-A2.
XX
PD 06-SEP-2002.
XX
PF 19-OCT-2001; 2001WO-US048350.
XX
PR 20-OCT-2000; 2000US-0242411P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
PA (BLAT/) BLATT L.
PA (MCSW/) MCSWIGGEN J A.
XX
PI Blatt L, Mcswiggen JA;
XX
DR WPI; 2002-706994/76.
XX
PT New nucleic acid molecule that modulates replication of West Nile Virus
PT (WNV), useful for treating a condition related to WNV infection e.g.
PT pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.
XX
PS Claim 23; SEQ ID NO 12004; 495pp; English.
XX
CC The invention relates to nucleic acid molecules that modulate replication
CC of the West Nile Virus (WNV). The nucleic acid molecules are useful for
CC treating a condition related to WNV infection e.g. pancreatitis,
CC encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,
CC liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid
CC molecule is selected from the group of ribozymes consisting of
CC Hammerhead, Inozyme, G-cleaver, DNAzyme, Amberzyme and Zinzyme. The
CC nucleic acid molecules further comprise at least five ribose residues, at
CC least ten 2'-O-methyl modifications, phosphorothioate linkages on at
CC least three of the 5' terminal nucleotides and a 3' end modification of a
CC 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080
CC are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given
CC in the specification. The present sequence is that of a nucleic acid
CC molecule of the invention
XX
SQ Sequence 17 BP; 4 A; 5 C; 2 G; 0 T; 6 U; 0 Other;

Query Match 61.0%; Score 12.2; DB 1; Length 17;
Best Local Similarity 52.9%; Pred. No. 20;
Matches 9; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Qy 3 TCATGGTCACATGGATG 19
:||: :|||| ||:|
Db 1 UCAUCUUCACAUCGAUG 17

RESULT 18
ACN70710/c
ID ACN70710 standard; DNA; 17 BP.
XX
AC ACN70710;
XX
DT 02-DEC-2004 (first entry)
XX
DE Human GDMLP-1 probe SEQ ID NO:7612.
XX
KW Human; ss; probe; myosin-like protein-1; hGDMLP-1;
KW hGDMLP-1 agonist hGDMLP antagonist; hGDMLP inhibitor; heart disorder;
KW skeletal muscle function.
XX
OS Homo sapiens.
XX
PN US2004137589-A1.
XX
PD 15-JUL-2004.
XX
PF 26-NOV-2003; 2003US-00723361.
XX
PR 26-MAY-2000; 2000US-0207456P.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
PR 30-JAN-2001; 2001WO-US000661.
PR 30-JAN-2001; 2001WO-US000662.
PR 30-JAN-2001; 2001WO-US000663.
PR 30-JAN-2001; 2001WO-US000664.
PR 30-JAN-2001; 2001WO-US000665.
PR 30-JAN-2001; 2001WO-US000666.
PR 30-JAN-2001; 2001WO-US000667.
PR 30-JAN-2001; 2001WO-US000668.
PR 30-JAN-2001; 2001WO-US000669.
PR 30-JAN-2001; 2001WO-US000670.

PR 05-FEB-2001; 2001US-0266860P.
PR 25-MAY-2001; 2001US-00866108.
XX
PA (GUYY/) GU Y.
PA (JIYY/) JI Y.
PA (PENN/) PENN S G.
PA (HANZ/) HANZEL D K.
PA (RANK/) RANK D.
PA (CHEN/) CHEN W.
PA (SHAN/) SHANNON M E.
XX
PI Gu Y, Ji Y, Penn SG, Hanzel DK, Rank D, Chen W, Shannon ME;
XX
DR WPI; 2004-533378/51.
XX
PT Novel myosin-like protein-1, useful for treating or preventing disorder
PT associated with decreased expression or activity of human genome-derived
PT myosin-like protein-1 such as disorder of heart and/or skeletal muscle
PT function.
XX
PS Disclosure; SEQ ID NO 7612; 0pp; English.
XX
CC The invention relates to a novel polypeptide (I) comprising a sequence
CC (S1) of myosin-like protein-1 (hGDMLP-1) having 2568 amino acids fully
CC defined in the specification, a fragment of at least 8 amino acids of
CC (S1), 95% deviation from (S1) which are conservative substitutions, and
CC 65% identity to (S1). A polypeptide of the invention acts as a agonist or
CC antagonist of hGDMLP-1, or as an inhibitor of hGDMLP-1 activity. A
CC pharmaceutical composition of the invention is useful for treating or
CC preventing a disorder associated with decreased expression or activity of
CC hGDMLP-1, such as a disorder of heart and/or skeletal muscle function.
CC The present sequence represents a 17-mer nucleotide, used in the
CC invention for scanning the sequence represented in ACN63103
XX
SQ Sequence 17 BP; 3 A; 4 C; 5 G; 5 T; 0 U; 0 Other;

Query Match 61.0%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 20;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CCTCATGGTCACATGGA 17
||||| ||||||| | |
Db 17 CCTCAAGGTCACAGGTA 1

RESULT 19
AAF51883/c
ID AAF51883 standard; DNA; 15 BP.
XX
AC AAF51883;
XX
DT 30-MAR-2001 (first entry)
XX
DE IGF-I oligonucleotide #2843.
XX
KW Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
KW cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;
KW skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;
KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
KW growth factor mediated cell proliferation; ichthyosis; serborrhoea; ruba;
KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
KW hyperneovascular condition; hyperplasia; kidney disease;
KW neovascular condition of the retina; ss.
XX
OS Homo sapiens.
XX
PN WO200078341-A1.
XX
PD 28-DEC-2000.
XX
PF 21-JUN-2000; 2000WO-AU000693.
XX
PR 21-JUN-1999; 99US-0140345P.
XX
PA (MURD-) MURDOCH CHILDRENS RES INST.
XX
PI Wraight CJ, Werther GA, Edmondson SR;
XX
DR WPI; 2001-041421/05.
XX
PT Ameliorating the effects of a disorder, e.g. psoriasis, by administering
PT UV (ultra-violet) treatment (optional) and an antisense nucleic acid that
PT inhibits or reduces growth factor mediated cell proliferation and/or
PT inflammation.
XX
PS Example 8; Page 79; 201pp; English.
XX
CC The present invention relates to a method for ameliorating the effects of
CC skin disorders. The method comprises contacting the skin with an
CC antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
CC inhibiting or reducing growth factor mediated cell proliferation,
CC inflammation and/or other disorders. The present sequence is an
CC oligonucleotide which can be used to design the antisense
CC oligonucleotides of the present invention (see AAF45151 and AAF45153-
CC F45161). The method is useful for ameliorating the effects of psoriasis,
CC ichthyosis, pityriasis, ruba, pilaris, serborrhoea, keloids, keratosis,
CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
CC hyperneovascular condition such as a neovascular condition of the retina,
CC brain or skin, growth factor-mediated malignancies, other sclerotic
CC disease, kidney disease, hyperproliferation of the inside of blood
CC vessels or any other hyperplasia
XX
SQ Sequence 15 BP; 4 A; 5 C; 1 G; 5 T; 0 U; 0 Other;

Query Match 59.0%; Score 11.8; DB 1; Length 15;
Best Local Similarity 86.7%; Pred. No. 18;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 6 TGGTCACATGGATGA 20
|| ||| ||||||||
Db 15 TGATCAGATGGATGA 1

RESULT 20
AAF51884/c
ID AAF51884 standard; DNA; 15 BP.
XX
AC AAF51884;
XX
DT 30-MAR-2001 (first entry)
XX
DE IGF-I oligonucleotide #2844.
XX
KW Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
KW cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;
KW skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;
KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
KW growth factor mediated cell proliferation; ichthyosis; serborrhoea; ruba;
KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
KW hyperneovascular condition; hyperplasia; kidney disease;
KW neovascular condition of the retina; ss.
XX
OS Homo sapiens.
XX
PN WO200078341-A1.
XX
PD 28-DEC-2000.
XX
PF 21-JUN-2000; 2000WO-AU000693.
XX
PR 21-JUN-1999; 99US-0140345P.
XX
PA (MURD-) MURDOCH CHILDRENS RES INST.
XX
PI Wraight CJ, Werther GA, Edmondson SR;

```
XX
DR   WPI; 2001-041421/05.
XX
PT   Ameliorating the effects of a disorder, e.g. psoriasis, by administering
PT   UV (ultra-violet) treatment (optional) and an antisense nucleic acid that
PT   inhibits or reduces growth factor mediated cell proliferation and/or
PT   inflammation.
XX
PS   Example 8; Page 79; 201pp; English.
XX
CC   The present invention relates to a method for ameliorating the effects of
CC   skin disorders. The method comprises contacting the skin with an
CC   antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
CC   receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
CC   inhibiting or reducing growth factor mediated cell proliferation,
CC   inflammation and/or other disorders. The present sequence is an
CC   oligonucleotide which can be used to design the antisense
CC   oligonucleotides of the present invention (see AAF45151 and AAF45153-
CC   F45161). The method is useful for ameliorating the effects of psoriasis,
CC   ichthyosis, pityriasis, ruba, pilaris, serborrhoea, keloids, keratosis,
CC   neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
CC   hyperneovascular condition such as a neovascular condition of the retina,
CC   brain or skin, growth factor-mediated malignancies, other sclerotic
CC   disease, kidney disease, hyperproliferation of the inside of blood
CC   vessels or any other hyperplasia
XX
SQ   Sequence 15 BP; 4 A; 5 C; 1 G; 5 T; 0 U; 0 Other;

  Query Match             59.0%;  Score 11.8;  DB 1;  Length 15;
  Best Local Similarity   86.7%;  Pred. No. 18;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          5 ATGGTCACATGGATG 19
              ||| ||| |||||||
Db         15 ATGATCAGATGGATG 1


RESULT 21
ADZ59539/c
ID   ADZ59539 standard; DNA; 16 BP.
XX
AC   ADZ59539;
XX
DT   30-JUN-2005  (first entry)
XX
DE   Hyperparathyroidism polymorphic detection VIC probe, SEQ ID 33.
XX
KW   secondary hyperparathyroidism; endocrine-gen.; antithyroid;
KW   renal failure; nephrotropic; SNP detection; ss; probe.
XX
OS   Synthetic.
XX
PN   JP2005102601-A.
XX
PD   21-APR-2005.
XX
PF   30-SEP-2003; 2003JP-00341015.
XX
PR   30-SEP-2003; 2003JP-00341015.
XX
PA   (HYUB-) HYUBITTO GENOMICS KK.
PA   (JIKE-) UNIV JIKEI.
XX
DR   WPI; 2005-358641/37.
XX
PT   Testing secondary hyperparathyroidism in chronic renal failure patient,
PT   involves detecting variation in gene chosen from CACNA1C, CALCRL, CHI3L1,
PT   EGF, FGF1, GFRA1, GPR56 and GPRK6.
XX
PS   Disclosure; SEQ ID NO 33; 138pp; Japanese.
XX
CC   The invention relates to a novel method for testing secondary
CC   hyperparathyroidism in a chronic renal failure patient. The method
CC   involves detecting a variation in a gene chosen from CACNA1C, CALCRL,
CC   CHI3L1, EGF, FGF1, GFRA1, GPR56, GPRK6, IL10RA, IL10RB, IL12RB1, KCNJ14,
CC   KCNQ1, ORCTL4, PDGFRA, SCYB14, SLC12A1, SLC2A3, TGFBR3, TMEM1, CALCR,
CC   IL17R, OSTF1, FGF6, HGF, MET, TGFB1 and VEGF, or detecting the base in a
CC   polymorphism region existing in the vicinity of any one of the genes. The
CC   invention further comprises a reagent or kit for testing secondary
CC   hyperparathyroidism in a chronic renal failure patient. This
CC   polynucleotide sequence represents a probe used in the detection of a
CC   polymorphism in a gene linked to secondary hyperparathyroidism of the
CC   invention.
XX
SQ   Sequence 16 BP; 4 A; 5 C; 3 G; 4 T; 0 U; 0 Other;

  Query Match             59.0%;  Score 11.8;  DB 1;  Length 16;
  Best Local Similarity   86.7%;  Pred. No. 20;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          3 TCATGGTCACATGGA 17
              || |||||||| |||
Db         16 TCTTGGTCACAGGGA 2


RESULT 22
ADZ59706/c
ID   ADZ59706 standard; DNA; 16 BP.
XX
AC   ADZ59706;
XX
DT   30-JUN-2005  (first entry)
XX
DE   Hyperparathyroidism polymorphic detection VIC probe, SEQ ID 200.
XX
KW   secondary hyperparathyroidism; endocrine-gen.; antithyroid;
KW   renal failure; nephrotropic; SNP detection; ss; probe.
XX
OS   Synthetic.
XX
PN   JP2005102601-A.
XX
PD   21-APR-2005.
XX
PF   30-SEP-2003; 2003JP-00341015.
XX
PR   30-SEP-2003; 2003JP-00341015.
XX
PA   (HYUB-) HYUBITTO GENOMICS KK.
PA   (JIKE-) UNIV JIKEI.
XX
DR   WPI; 2005-358641/37.
XX
PT   Testing secondary hyperparathyroidism in chronic renal failure patient,
PT   involves detecting variation in gene chosen from CACNA1C, CALCRL, CHI3L1,
PT   EGF, FGF1, GFRA1, GPR56 and GPRK6.
XX
PS   Disclosure; SEQ ID NO 200; 138pp; Japanese.
XX
CC   The invention relates to a novel method for testing secondary
CC   hyperparathyroidism in a chronic renal failure patient. The method
CC   involves detecting a variation in a gene chosen from CACNA1C, CALCRL,
CC   CHI3L1, EGF, FGF1, GFRA1, GPR56, GPRK6, IL10RA, IL10RB, IL12RB1, KCNJ14,
CC   KCNQ1, ORCTL4, PDGFRA, SCYB14, SLC12A1, SLC2A3, TGFBR3, TMEM1, CALCR,
CC   IL17R, OSTF1, FGF6, HGF, MET, TGFB1 and VEGF, or detecting the base in a
CC   polymorphism region existing in the vicinity of any one of the genes. The
CC   invention further comprises a reagent or kit for testing secondary
CC   hyperparathyroidism in a chronic renal failure patient. This
CC   polynucleotide sequence represents a probe used in the detection of a
CC   polymorphism in a gene linked to secondary hyperparathyroidism of the
CC   invention.
XX
SQ   Sequence 16 BP; 4 A; 5 C; 3 G; 4 T; 0 U; 0 Other;

  Query Match             59.0%;  Score 11.8;  DB 1;  Length 16;
  Best Local Similarity   86.7%;  Pred. No. 20;
```

```
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          3 TCATGGTCACATGGA 17
              || |||||||| |||
Db         16 TCTTGGTCACAGGGA 2


RESULT 23
ADG13603
ID   ADG13603 standard; RNA; 15 BP.
XX
AC   ADG13603;
XX
DT   26-FEB-2004  (first entry)
XX
DE   Human HER1-4 hammerhead ribozyme target sequence #3.
XX
KW   Human; ss; EGFR; epidermal growth factor receptor; HER1; HER2; HER3;
KW   HER4; hammerhead ribozyme; inozyme; zinzyme; DNAzyme; amberzyme; cancer;
KW   brain tumour; cytostatic; short interfering RNA; siRNA; RNA interference;
KW   prostate cancer; colorectal cancer; brain cancer; oesophageal cancer;
KW   stomach cancer; bladder cancer; pancreatic cancer; cervical cancer;
KW   head and neck cancer; ovarian cancer; melanoma; lymphoma; glioma;
KW   multidrug resistant cancer.
XX
OS   Homo sapiens.
XX
PN   US2003186909-A1.
XX
PD   02-OCT-2003.
XX
PF   21-OCT-2002; 2002US-00277494.
XX
PR   27-JAN-1997;   97US-0036749P.
PR   04-DEC-1997;   97US-00985162.
PR   22-SEP-1999;   99US-00401063.
PR   03-MAY-2001; 2001US-00848754.
PR   25-JUL-2001; 2001US-00916466.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J;
XX
DR   WPI; 2004-032029/03.
XX
PT   New double stranded short interfering ribonucleic acid molecule for
PT   inhibiting expression of epidermal growth factor receptor gene.
XX
PS   Claim 7; SEQ ID NO 30; 113pp; English.
XX
CC   The invention relates to a double stranded short interfering RNA (siRNA)
CC   molecule that inhibits expression of epidermal growth factor receptor
CC   (EGFR) gene (e.g. HER1-4) by RNA interference is new. Also included is an
CC   expression vector comprising a nucleic acid sequence encoding siRNA
CC   molecule(s) in a manner that allows expression of the nucleic acid
CC   molecule. The siRNA molecules comprise hammerhead ribozymes, inozymes,
CC   amberzymes zinzymes and DNAzymes. The invention is used for inhibiting
CC   expression of EGFR. It can be used for treatment of cancer, prostate
CC   cancer, colorectal cancer, brain cancer, oesophageal cancer, stomach
CC   cancer, bladder cancer, pancreatic cancer, cervical cancer, head and neck
CC   cancer, ovarian cancer, melanoma, lymphoma, glioma, multidrug resistant
CC   cancer or a brain tumour. The invention has enhanced shelf-life, half-
CC   life in vitro , stability, and ease of introduction of oligonucleotide to
CC   target site. The present sequence is an EGFR/HER1-4 target sequence for
CC   an siRNA of the invention.
XX
SQ   Sequence 15 BP; 4 A; 2 C; 3 G; 0 T; 6 U; 0 Other;

  Query Match             57.0%;  Score 11.4;  DB 1;  Length 15;
  Best Local Similarity   61.5%;  Pred. No. 21;
  Matches    8;  Conservative    4;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 TCATGGTCACATG 15
              :||:||:|| |:|
Db          1 UCAUGGUCAAAUG 13


RESULT 24
ADM69289/c
ID   ADM69289 standard; DNA; 16 BP.
XX
AC   ADM69289;
XX
DT   03-JUN-2004  (first entry)
XX
DE   Plant gene polymorphism marker related primer, SEQ ID 168.
XX
KW   Primer; variation mapping; mutation mapping; plant;
KW   gene polymorphism marker; ss.
XX
OS   Synthetic.
XX
PN   JP2003289885-A.
XX
PD   14-OCT-2003.
XX
PF   31-JAN-2003; 2003JP-00024620.
XX
PR   01-FEB-2002; 2002JP-00025338.
XX
PA   (RIKA ) RIKAGAKU KENKYUSHO.
PA   (SAIM-) SAI MEDIA KK.
PA   (MATS/) MATSUI M.
PA   (NAKA/) NAKAZAWA M.
XX
DR   WPI; 2004-126231/13.
XX
PT   A primer set and method useful for mapping at least the
PT   variation/mutation part of a plant gene using a gene polymorphism marker.
XX
PS   Claim 7; SEQ ID NO 168; 120pp; Japanese.
XX
CC   The present invention relates to a primer set and method for mapping at
CC   least the variation/mutation part of a plant gene using a gene
CC   polymorphism marker. A mutation site of the plant gene is mapped by
CC   utilizing a genetic polymorphism marker as follows: (a) genomic DNA is
CC   prepared from a plant homozygously having a mutation to be an object of
CC   the mapping; (b) A forward primer 1 containing a base corresponding to
CC   the gene polymorphic maker of one ecotype plant, a forward primer 2
CC   containing a base corresponding to the genetic polymorphism of the other
CC   ecotype plant and a reverse primer 3 based on the base sequence common
CC   with both the ecotype plants are prepared; (c) two kinds of
CC   oligonucleotides emitting fluorescence of different colors when the
CC   genetic polymorphism marker is detected are prepared; (d) an
CC   amplification reaction of the genomic DNA is carried out in the presence
CC   of the primers 1, 2 and 3 and the two kinds of the oligonucleotides; (e)
CC   the fluorescence intensity emitted from the resultant reactional product
CC   is detected and (f) the position on the genome of the mutation site is
CC   determined from the results of detection. The present sequence is a
CC   primer, used to illustrate the invention.
XX
SQ   Sequence 16 BP; 2 A; 7 C; 3 G; 4 T; 0 U; 0 Other;

  Query Match             57.0%;  Score 11.4;  DB 1;  Length 16;
  Best Local Similarity   92.3%;  Pred. No. 23;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          8 GTCACATGGATGA 20
              |||||||||| ||
Db         14 GTCACATGGAGGA 2


RESULT 25
ADR74253/c
ID   ADR74253 standard; DNA; 16 BP.
XX
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AC   ADR74253;
XX
DT   16-DEC-2004  (first entry)
XX
DE   Common primer B for human MI-associated marker hCV2633049.
XX
KW   Human; ss; PCR; primer; SNP; single nucleotide polymorphism;
KW   myocardial infarction.
XX
OS   Homo sapiens.
XX
PN   WO2004081187-A2.
XX
PD   23-SEP-2004.
XX
PF   10-MAR-2004; 2004WO-US007141.
XX
PR   10-MAR-2003; 2003US-0453135P.
PR   30-APR-2003; 2003US-0466412P.
XX
PA   (APPL-) APPLERA CORP.
XX
PI   Cargill M,  Devlin JJ,  Iakoubova O,  Shiffman D;
XX
DR   WPI; 2004-677537/66.
XX
PT   Identifying an individual who has altered risk for developing myocardial
PT   infarction comprises detecting single nucleotide polymorphism (SNP), in
PT   the individual's nucleic acids.
XX
PS   Claim 19; SEQ ID NO 44078; 139pp; English.
XX
CC   The invention relates to identifying an individual who has altered risk
CC   for developing myocardial infarction comprises detecting single
CC   nucleotide polymorphism (SNP) in any one of the 43336 nucleotide
CC   sequences (not given in the specification), in the individual's nucleic
CC   acids, where the presence of the SNP is correlated with an altered risk
CC   for myocardial infarction in the individual. Also included are an
CC   isolated nucleic acid molecule (comprising at least 8 contiguous
CC   nucleotides where one of the nucleotides is an SNP as cited above, or
CC   their complement), an isolated polypeptide comprising an amino acid
CC   sequence selected from any of the 696 amino acid sequences not defined in
CC   the specification, an antibody that specifically binds to the polypeptide
CC   (or its antigen-binding fragment), an amplified polynucleotide containing
CC   the SNP as cited (where the amplified polynucleotide is between about 16
CC   and about 1,000 nucleotides in length), an isolated polynucleotide which
CC   specifically hybridises to a nucleic acid molecule containing the SNP, a
CC   kit for detecting SNP in a nucleic acid, detecting SNP in a nucleic acid
CC   molecule, detecting a variant polypeptide and identifying an agent useful
CC   in therapeutically or prophylactically treating myocardial infarction.
CC   The detection step of the method is carried out by a process selected
CC   from allele-specific probe hybridisation, allele-specific primer
CC   extension, allele-specific amplification, sequencing, 5' nuclease
CC   digestion, molecular beacon assay, oligonucleotide ligation assay, size
CC   analysis, and single-stranded conformation polymorphism. The method is
CC   useful for identifying an individual who has altered risk for developing
CC   myocardial infarction. The present sequence is common primer (used with
CC   an allele specific PCR primer) used to amplify an SNP-containing region
CC   from a myocardial infarction-associated marker gene. NOTE: SEQ IDs 1-
CC   43787 are not shown in the specification and are not available from WIPO.
CC   These sequence are contained on a CD-R named CL001509CDR which has not
CC   been supplied with the specification.
XX
SQ   Sequence 16 BP; 4 A; 6 C; 4 G; 2 T; 0 U; 0 Other;

  Query Match             56.0%;  Score 11.2;  DB 1;  Length 16;
  Best Local Similarity   81.2%;  Pred. No. 25;
  Matches   13;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 CCTCATGGTCACATGG 16
              | |||||| ||| |||
Db         16 CTTCATGGGCACGTGG 1
```

```
RESULT 26
ABK09404
ID   ABK09404 standard; DNA; 15 BP.
XX
AC   ABK09404;
XX
DT   14-MAR-2002  (first entry)
XX
DE   Human NPR1 gene allele-specific oligonucleotide sequencing primer #26.
XX
KW   Human; natriuretic peptide receptor A/guanylate cyclase A; NPR1; ss;
KW   atrionatriuretic peptide receptor A; haplotyping; cytostatic; genotyping;
KW   haplotype pair; single nucleotide polymorphism; gene therapy; PCR primer;
KW   drug screening; hypertension; hypotensive; sequencing primer; probe.
XX
OS   Homo sapiens.
XX
PN   WO200179231-A2.
XX
PD   25-OCT-2001.
XX
PF   16-APR-2001; 2001WO-US012300.
XX
PR   14-APR-2000; 2000US-0197330P.
XX
PA   (GENA-) GENAISSANCE PHARM INC.
XX
PI   Bentivegna SC,  Choi JY,  Kliem SE,  Nandabalan K;
XX
DR   WPI; 2002-066340/09.
XX
PT   Genotyping human natriuretic peptide receptor A/guanylate cyclase gene of
PT   an individual, involves determining identity of nucleotide pair at
PT   specific polymorphic sites for two copies of the gene.
XX
PS   Claim 15; Page 14; 96pp; English.
XX
CC   The invention relates to single nucleotide polymorphisms in the gene
CC   encoding the human natriuretic peptide receptor A/guanylate cyclase A
CC   (atrionatriuretic peptide receptor A) or NPR1 polypeptide. A method for
CC   haplotyping the NPR1 gene in an individual comprises identifying the
CC   nucleotide at one or more polymorphic sites and determining whether one
CC   of the copies of the gene is defined by one of the NPR1 haplotypes given
CC   in the specification or whether both copies are defined by a haplotype
CC   pair. This method is useful in genotyping, whereby all possible haplotype
CC   pairs can be assigned to specific genotypes. An association between a
CC   trait and a haplotype or haplotype pair of the NPR1 gene can be
CC   identified by comparing the frequency of the haplotype or haplotype pair
CC   in a population exhibiting the trait with the frequency of the haplotype
CC   or haplotype pair in a reference population, where a higher haplotype
CC   frequency in the trait population indicates the trait is associated with
CC   the haplotype or haplotype pair. NPR1 and its corresponding DNA are used
CC   for studying the expression and function of NPR1, for use in screening
CC   for candidate drugs to treat diseases related to NPR1 activity, such as
CC   hypertension. The sequences are also useful for studying the effect of
CC   variation on the biological activity of NPR1 as well as on the binding
CC   affinity of candidate drugs targeting NPR1. Sequences AAS99959-AAS99990
CC   and ABK09390-ABK09462 represent probes, sequencing primers and PCR
CC   primers used to detect NPR1 gene polymorphisms
XX
SQ   Sequence 15 BP; 5 A; 4 C; 3 G; 2 T; 0 U; 1 Other;

  Query Match             55.0%;  Score 11;  DB 1;  Length 15;
  Best Local Similarity   84.6%;  Pred. No. 24;
  Matches   11;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 CTCATGGTCACAT 14
              |||| |||||||:
Db          2 CTCAAGGTCACAY 14
```

```
RESULT 27
```

ACL73850
ID ACL73850 standard; DNA; 15 BP.
XX
AC ACL73850;
XX
DT 16-JUN-2005 (first entry)
XX
DE SARS coronavirus right PCR primer, SEQ:631.
XX
KW Vaccine; nucleic acid vaccine; drug screening; diagnosis;
KW SARS coronavirus infection; infection; respiratory disease; virucide;
KW PCR; primer; ss.
XX
OS SARS coronavirus.
XX
PN WO2004092360-A2.
XX
PD 28-OCT-2004.
XX
PF 09-APR-2004; 2004WO-US011710.
XX
PR 10-APR-2003; 2003US-0462218P.
PR 11-APR-2003; 2003US-0462465P.
PR 12-APR-2003; 2003US-0462418P.
PR 13-APR-2003; 2003US-0462748P.
PR 14-APR-2003; 2003US-0463109P.
PR 15-APR-2003; 2003US-0463460P.
PR 16-APR-2003; 2003US-0463668P.
PR 17-APR-2003; 2003US-0463983P.
PR 18-APR-2003; 2003US-0463971P.
PR 22-APR-2003; 2003US-0464838P.
PR 22-APR-2003; 2003US-0464899P.
PR 23-APR-2003; 2003US-0465273P.
PR 24-APR-2003; 2003US-0465535P.
PR 05-MAY-2003; 2003US-0468312P.
PR 22-MAY-2003; 2003US-0473144P.
PR 14-AUG-2003; 2003US-0495024P.
PR 23-SEP-2003; 2003US-0505652P.
PR 11-OCT-2003; 2003US-0510781P.
PR 11-DEC-2003; 2003US-0529464P.
PR 12-JAN-2004; 2004US-0536177P.
PR 07-APR-2004; 2004US-0560757P.
XX
PA (CHIR) CHIRON CORP.
XX
PI Rappuoli R, Masignani V, Stadler K, Gregersen J, Chien D, Han J;
PI Polo J, Weiner A, Houghton M, Song HC, Seo MY, Donnelly JJ;
PI Klenk HD, Valiante N;
XX
DR WPI; 2004-766863/75.
XX
PT Novel isolated polypeptide e.g. spike polypeptide, Env polypeptide, of
PT severe acute respiratory syndrome virus (SARS), useful as vaccine for
PT SARS.
XX
PS Claim 59; SEQ ID NO 631; 839pp; English.
XX
CC The invention relates to isolated polypeptides of the severe acute
CC respiratory syndrome (SARS) coronavirus. The polypeptides include spike
CC (S or E2), env (E or sM), membrane (M or E1), hemagglutinin-esterase (HE
CC or E3), and nucleocapsid (N) polypeptides, and the ORF1a and ORF1ab
CC (replicase) polypeptides and their proteolytic fragments. The invention
CC also relates to antibodies which recognise the polypeptides; nucleic
CC acids encoding the SARS virus polypeptides; primers specific for SARS
CC virus nucleic acid sequences; kits for amplifying SARS virus target
CC nucleic acids; a double-stranded RNA molecule 10-30 nucleotides in length
CC which is able to inactivate the SARS virus in a mammalian cell; an
CC expression construct for recombinant expression of a SARS virus spike
CC protein; a viral vector for in vivo delivery of a SARS virus polypeptide-
CC encoding nucleic acid; and a mammalian cell line stably expressing a SARS
CC viral antigen. The invention additionally provides a vaccine for the
CC treatment or prevention of SARS comprising an inactivated SARS virus, a
CC killed SARS virus, an attenuated SARS virus, a split SARS virus
CC preparation, or at least one purified SARS virus antigens; methods of
CC making inactivated SARS virus and vaccines containing it; an alpha-virus
CC replicon particle comprising one or more SARS viral antigens; and a
CC vaccine comprising one or more SARS virus antigens and one or more
CC respiratory virus antigens. The invention further encompasses a method of
CC identifying a therapeutically active agent by measuring the effect of the
CC agent on a SARS-related enzyme, and a method of treating a SARS patient
CC using small molecule viral inhibitors. The SARS virus polypeptides and
CC nucleic acids can be used in the preparation and manufacture of vaccines
CC for the treatment or prevention of SARS. The SARS virus polypeptides,
CC antibodies against them, and SARS virus-specific primers and kits
CC containing them are useful for diagnosing or identifying the presence of
CC SARS in a biological sample. The present sequence represents a PCR primer
CC for amplifying a SARS coronavirus gene. Note: The sequence data for this
CC patent did not form part of the printed specification, but was obtained
CC in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 15 BP; 3 A; 5 C; 3 G; 4 T; 0 U; 0 Other;

Query Match 55.0%; Score 11; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 CTCATGGTCAC 12
||||||||||
Db 5 CTCATGGTCAC 15

RESULT 28
ACL73880
ID ACL73880 standard; DNA; 15 BP.
XX
AC ACL73880;
XX
DT 16-JUN-2005 (first entry)
XX
DE SARS coronavirus right PCR primer, SEQ:661.
XX
KW Vaccine; nucleic acid vaccine; drug screening; diagnosis;
KW SARS coronavirus infection; infection; respiratory disease; virucide;
KW PCR; primer; ss.
XX
OS SARS coronavirus.
XX
PN WO2004092360-A2.
XX
PD 28-OCT-2004.
XX
PF 09-APR-2004; 2004WO-US011710.
XX
PR 10-APR-2003; 2003US-0462218P.
PR 11-APR-2003; 2003US-0462465P.
PR 12-APR-2003; 2003US-0462418P.
PR 13-APR-2003; 2003US-0462748P.
PR 14-APR-2003; 2003US-0463109P.
PR 15-APR-2003; 2003US-0463460P.
PR 16-APR-2003; 2003US-0463668P.
PR 17-APR-2003; 2003US-0463983P.
PR 18-APR-2003; 2003US-0463971P.
PR 22-APR-2003; 2003US-0464838P.
PR 22-APR-2003; 2003US-0464899P.
PR 23-APR-2003; 2003US-0465273P.
PR 24-APR-2003; 2003US-0465535P.
PR 05-MAY-2003; 2003US-0468312P.
PR 22-MAY-2003; 2003US-0473144P.
PR 14-AUG-2003; 2003US-0495024P.
PR 23-SEP-2003; 2003US-0505652P.
PR 11-OCT-2003; 2003US-0510781P.
PR 11-DEC-2003; 2003US-0529464P.
PR 12-JAN-2004; 2004US-0536177P.
PR 07-APR-2004; 2004US-0560757P.
XX

PA (CHIR) CHIRON CORP.
XX
PI Rappuoli R, Masignani V, Stadler K, Gregersen J, Chien D, Han J;
PI Polo J, Weiner A, Houghton M, Song HC, Seo MY, Donnelly JJ;
PI Klenk HD, Valiante N;
XX
DR WPI; 2004-766863/75.
XX
PT Novel isolated polypeptide e.g. spike polypeptide, Env polypeptide, of
PT severe acute respiratory syndrome virus (SARS), useful as vaccine for
PT SARS.
XX
PS Claim 59; SEQ ID NO 661; 839pp; English.
XX
CC The invention relates to isolated polypeptides of the severe acute
CC respiratory syndrome (SARS) coronavirus. The polypeptides include spike
CC (S or E2), env (E or sM), membrane (M or E1), hemagglutinin-esterase (HE
CC or E3), and nucleocapsid (N) polypeptides, and the ORF1a and ORF1ab
CC (replicase) polypeptides and their proteolytic fragments. The invention
CC also relates to antibodies which recognise the polypeptides; nucleic
CC acids encoding the SARS virus polypeptides; primers specific for SARS
CC virus nucleic acid sequences; kits for amplifying SARS virus target
CC nucleic acids; a double-stranded RNA molecule 10-30 nucleotides in length
CC which is able to inactivate the SARS virus in a mammalian cell; an
CC expression construct for recombinant expression of a SARS virus spike
CC protein; a viral vector for in vivo delivery of a SARS virus polypeptide-
CC encoding nucleic acid; and a mammalian cell line stably expressing a SARS
CC viral antigen. The invention additionally provides a vaccine for the
CC treatment or prevention of SARS comprising an inactivated SARS virus, a
CC killed SARS virus, an attenuated SARS virus, a split SARS virus
CC preparation, or at least one purified SARS virus antigens; methods of
CC making inactivated SARS virus and vaccines containing it; an alpha-virus
CC replicon particle comprising one or more SARS viral antigens; and a
CC vaccine comprising one or more SARS virus antigens and one or more
CC respiratory virus antigens. The invention further encompasses a method of
CC identifying a therapeutically active agent by measuring the effect of the
CC agent on a SARS-related enzyme, and a method of treating a SARS patient
CC using small molecule viral inhibitors. The SARS virus polypeptides and
CC nucleic acids can be used in the preparation and manufacture of vaccines
CC for the treatment or prevention of SARS. The SARS virus polypeptides,
CC antibodies against them, and SARS virus-specific primers and kits
CC containing them are useful for diagnosing or identifying the presence of
CC SARS in a biological sample. The present sequence represents a PCR primer
CC for amplifying a SARS coronavirus gene. Note: The sequence data for this
CC patent did not form part of the printed specification, but was obtained
CC in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 15 BP; 3 A; 5 C; 4 G; 3 T; 0 U; 0 Other;

Query Match 55.0%; Score 11; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 CTCATGGTCAC 12
||||||||||
Db 1 CTCATGGTCAC 11

RESULT 29
ACL73792
ID ACL73792 standard; DNA; 15 BP.
XX
AC ACL73792;
XX
DT 16-JUN-2005 (first entry)
XX
DE SARS coronavirus right PCR primer, SEQ:573.
XX
KW Vaccine; nucleic acid vaccine; drug screening; diagnosis;
KW SARS coronavirus infection; infection; respiratory disease; virucide;
KW PCR; primer; ss.
XX
OS SARS coronavirus.
XX
PN WO2004092360-A2.
XX
PD 28-OCT-2004.
XX
PF 09-APR-2004; 2004WO-US011710.
XX
PR 10-APR-2003; 2003US-0462218P.
PR 11-APR-2003; 2003US-0462465P.
PR 12-APR-2003; 2003US-0462418P.
PR 13-APR-2003; 2003US-0462748P.
PR 14-APR-2003; 2003US-0463109P.
PR 15-APR-2003; 2003US-0463460P.
PR 16-APR-2003; 2003US-0463668P.
PR 17-APR-2003; 2003US-0463983P.
PR 18-APR-2003; 2003US-0463971P.
PR 22-APR-2003; 2003US-0464838P.
PR 22-APR-2003; 2003US-0464899P.
PR 23-APR-2003; 2003US-0465273P.
PR 24-APR-2003; 2003US-0465535P.
PR 05-MAY-2003; 2003US-0468312P.
PR 22-MAY-2003; 2003US-0473144P.
PR 14-AUG-2003; 2003US-0495024P.
PR 23-SEP-2003; 2003US-0505652P.
PR 11-OCT-2003; 2003US-0510781P.
PR 11-DEC-2003; 2003US-0529464P.
PR 12-JAN-2004; 2004US-0536177P.
PR 07-APR-2004; 2004US-0560757P.
XX
PA (CHIR) CHIRON CORP.
XX
PI Rappuoli R, Masignani V, Stadler K, Gregersen J, Chien D, Han J;
PI Polo J, Weiner A, Houghton M, Song HC, Seo MY, Donnelly JJ;
PI Klenk HD, Valiante N;
XX
DR WPI; 2004-766863/75.
XX
PT Novel isolated polypeptide e.g. spike polypeptide, Env polypeptide, of
PT severe acute respiratory syndrome virus (SARS), useful as vaccine for
PT SARS.
XX
PS Claim 59; SEQ ID NO 573; 839pp; English.
XX
CC The invention relates to isolated polypeptides of the severe acute
CC respiratory syndrome (SARS) coronavirus. The polypeptides include spike
CC (S or E2), env (E or sM), membrane (M or E1), hemagglutinin-esterase (HE
CC or E3), and nucleocapsid (N) polypeptides, and the ORF1a and ORF1ab
CC (replicase) polypeptides and their proteolytic fragments. The invention
CC also relates to antibodies which recognise the polypeptides; nucleic
CC acids encoding the SARS virus polypeptides; primers specific for SARS
CC virus nucleic acid sequences; kits for amplifying SARS virus target
CC nucleic acids; a double-stranded RNA molecule 10-30 nucleotides in length
CC which is able to inactivate the SARS virus in a mammalian cell; an
CC expression construct for recombinant expression of a SARS virus spike
CC protein; a viral vector for in vivo delivery of a SARS virus polypeptide-
CC encoding nucleic acid; and a mammalian cell line stably expressing a SARS
CC viral antigen. The invention additionally provides a vaccine for the
CC treatment or prevention of SARS comprising an inactivated SARS virus, a
CC killed SARS virus, an attenuated SARS virus, a split SARS virus
CC preparation, or at least one purified SARS virus antigens; methods of
CC making inactivated SARS virus and vaccines containing it; an alpha-virus
CC replicon particle comprising one or more SARS viral antigens; and a
CC vaccine comprising one or more SARS virus antigens and one or more
CC respiratory virus antigens. The invention further encompasses a method of
CC identifying a therapeutically active agent by measuring the effect of the
CC agent on a SARS-related enzyme, and a method of treating a SARS patient
CC using small molecule viral inhibitors. The SARS virus polypeptides and
CC nucleic acids can be used in the preparation and manufacture of vaccines
CC for the treatment or prevention of SARS. The SARS virus polypeptides,
CC antibodies against them, and SARS virus-specific primers and kits
CC containing them are useful for diagnosing or identifying the presence of
CC SARS in a biological sample. The present sequence represents a PCR primer

```
CC   for amplifying a SARS coronavirus gene. Note: The sequence data for this
CC   patent did not form part of the printed specification, but was obtained
CC   in electronic format directly from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 15 BP; 3 A; 4 C; 4 G; 4 T; 0 U; 0 Other;

  Query Match             55.0%;  Score 11;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 24;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 CTCATGGTCAC 12
              ||||||||||| |
Db          4 CTCATGGTCAC 14


RESULT 30
ADL96404
ID   ADL96404 standard; DNA; 14 BP.
XX
AC   ADL96404;
XX
DT   20-MAY-2004  (first entry)
XX
DE   Acute myeloid leukaemia (AML) associated EST seqid 303.
XX
KW   cytostatic; gene therapy; microarray; gene expression characteristic;
KW   haematopoietic cell; haematopoiesis; myeloid leukaemia; EST;
KW   expressed sequence tag; acute myeloid leukaemia; AML; translocation; t(9;
KW   11); ss.
XX
OS   Homo sapiens.
XX
PN   US2003165949-A1.
XX
PD   04-SEP-2003.
XX
PF   23-DEC-2002; 2002US-00329465.
XX
PR   27-DEC-2001; 2001US-0343826P.
XX
PA   (WANG/) WANG S M.
PA   (LEES/) LEE S.
PA   (CHEN/) CHEN J.
PA   (ZHOU/) ZHOU G.
PA   (ROWL/) ROWLEY J D.
XX
PI   Wang SM,  Lee S,  Chen J,  Zhou G,  Rowley JD;
XX
DR   WPI; 2003-863699/80.
XX
PT   New microarray for measuring gene expression characteristics of
PT   hematopoietic cells, useful for preparing a composition for diagnosing or
PT   treating myeloid leukemia.
XX
PS   Example 3; SEQ ID NO 303; 32pp; English.
XX
CC   The invention describes a microarray for measuring gene expression
CC   characteristics of haematopoietic cells comprising at least 5
CC   polynucleotides having distinct sequences. Also described are: a method
CC   of diagnosing or treating an abnormality associated with haematopoiesis;
CC   and diagnosing myeloid leukaemia in a patient. The microarray is useful
CC   for preparing a composition for diagnosing or treating myeloid leukaemia.
CC   This sequence represents an expressed sequence tag (EST) isolated from a
CC   cell of a patient with acute myeloid leukaemia with the t(9;11)
CC   translocation that results in the mixed-lineage leukaemia (MML)-AF9
CC   fusion protein.
XX
SQ   Sequence 14 BP; 6 A; 2 C; 4 G; 2 T; 0 U; 0 Other;

  Query Match             54.0%;  Score 10.8;  DB 1;  Length 14;
  Best Local Similarity   85.7%;  Pred. No. 22;
  Matches   12;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          4 CATGGTCACATGGA 17
              |||||||| | |||
Db          1 CATGGTCAAAAGGA 14


RESULT 31
AAX31458
ID   AAX31458 standard; DNA; 15 BP.
XX
AC   AAX31458;
XX
DT   21-MAY-1999  (first entry)
XX
DE   Tag sequence of a transcript decreased in colorectal cancer.
XX
KW   Tag sequence; colorectal cancer; pancreatic cancer; colon cancer;
KW   diagnosis; prognosis; treatment; ss.
XX
OS   Homo sapiens.
XX
PN   WO9853319-A2.
XX
PD   26-NOV-1998.
XX
PF   20-MAY-1998;   98WO-US010277.
XX
PR   21-MAY-1997;   97US-0047352P.
XX
PA   (UYJO ) UNIV JOHNS HOPKINS.
XX
PI   Vogelstein B,  Kinzler KW;
XX
DR   WPI; 1999-070161/06.
XX
PT   Use of isolated gene transcripts - useful for developing products for the
PT   diagnosis, prognosis and treatment of cancers, particularly colon and
PT   pancreatic cancer.
XX
PS   Claim 1; Page 51; 120pp; English.
XX
CC   AAX30947-31815 represent tag sequences of transcripts that are
CC   differentially expressed in colorectal cancer, in pancreatic cancer, or
CC   in both. The tag sequences can be used to identify genes by matching the
CC   tag to a gen data base member, or by using the tag sequences as probes to
CC   isolate unidentified genes from cDNA libraries. The tag sequences can
CC   also be used in a method for diagnosing colon or pancreatic cancer in a
CC   sample suspected of being neoplastic. The method comprises comparing the
CC   level of at least one transcript in a first sample of a tissue to a
CC   second sample, where the first sample is a colonic tissue suspected of
CC   being neoplastic and the second sample is a normal human colonic tissue.
CC   The transcript is identified by a tag selected from AAX30947-31815. The
CC   methods of the invention can be used in the diagnosis, prognosis and
CC   treatment of cancer
XX
SQ   Sequence 15 BP; 3 A; 4 C; 6 G; 2 T; 0 U; 0 Other;

  Query Match             54.0%;  Score 10.8;  DB 1;  Length 15;
  Best Local Similarity   85.7%;  Pred. No. 25;
  Matches   12;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          4 CATGGTCACATGGA 17
              ||||| ||| ||||
Db          1 CATGGCCACGTGGA 14


RESULT 32
AAF51885/c
ID   AAF51885 standard; DNA; 15 BP.
XX
AC   AAF51885;
XX
DT   30-MAR-2001  (first entry)
```

```
XX
DE   IGF-I oligonucleotide #2845.
XX
KW   Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
KW   cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;
KW   skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;
KW   IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
KW   growth factor mediated cell proliferation; ichthyosis; serborrhoea; ruba;
KW   keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
KW   hyperneovascular condition; hyperplasia; kidney disease;
KW   neovascular condition of the retina; ss.
XX
OS   Homo sapiens.
XX
PN   WO200078341-A1.
XX
PD   28-DEC-2000.
XX
PF   21-JUN-2000; 2000WO-AU000693.
XX
PR   21-JUN-1999;   99US-0140345P.
XX
PA   (MURD-) MURDOCH CHILDRENS RES INST.
XX
PI   Wraight CJ,  Werther GA,  Edmondson SR;
XX
DR   WPI; 2001-041421/05.
XX
PT   Ameliorating the effects of a disorder, e.g. psoriasis, by administering
PT   UV (ultra-violet) treatment (optional) and an antisense nucleic acid that
PT   inhibits or reduces growth factor mediated cell proliferation and/or
PT   inflammation.
XX
PS   Example 8; Page 79; 201pp; English.
XX
CC   The present invention relates to a method for ameliorating the effects of
CC   skin disorders. The method comprises contacting the skin with an
CC   antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
CC   receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
CC   inhibiting or reducing growth factor mediated cell proliferation,
CC   inflammation and/or other disorders. The present sequence is an
CC   oligonucleotide which can be used to design the antisense
CC   oligonucleotides of the present invention (see AAF45151 and AAF45153-
CC   F45161). The method is useful for ameliorating the effects of psoriasis,
CC   ichthyosis, pityriasis, ruba, pilaris, serborrhoea, keloids, keratosis,
CC   neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
CC   hyperneovascular condition such as a neovascular condition of the retina,
CC   brain or skin, growth factor-mediated malignancies, other sclerotic
CC   disease, kidney disease, hyperproliferation of the inside of blood
CC   vessels or any other hyperplasia
XX
SQ   Sequence 15 BP; 4 A; 5 C; 1 G; 5 T; 0 U; 0 Other;

  Query Match             54.0%;  Score 10.8;  DB 1;  Length 15;
  Best Local Similarity   85.7%;  Pred. No. 25;
  Matches   12;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          5 ATGGTCACATGGAT 18
              ||| ||| ||||||
Db         14 ATGATCAGATGGAT 1


RESULT 33
AAF51882/c
ID   AAF51882 standard; DNA; 15 BP.
XX
AC   AAF51882;
XX
DT   30-MAR-2001  (first entry)
XX
DE   IGF-I oligonucleotide #2842.
XX
KW   Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
KW   cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;
KW   skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;
KW   IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
KW   growth factor mediated cell proliferation; ichthyosis; serborrhoea; ruba;
KW   keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
KW   hyperneovascular condition; hyperplasia; kidney disease;
KW   neovascular condition of the retina; ss.
XX
OS   Homo sapiens.
XX
PN   WO200078341-A1.
XX
PD   28-DEC-2000.
XX
PF   21-JUN-2000; 2000WO-AU000693.
XX
PR   21-JUN-1999;   99US-0140345P.
XX
PA   (MURD-) MURDOCH CHILDRENS RES INST.
XX
PI   Wraight CJ,  Werther GA,  Edmondson SR;
XX
DR   WPI; 2001-041421/05.
XX
PT   Ameliorating the effects of a disorder, e.g. psoriasis, by administering
PT   UV (ultra-violet) treatment (optional) and an antisense nucleic acid that
PT   inhibits or reduces growth factor mediated cell proliferation and/or
PT   inflammation.
XX
PS   Example 8; Page 79; 201pp; English.
XX
CC   The present invention relates to a method for ameliorating the effects of
CC   skin disorders. The method comprises contacting the skin with an
CC   antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
CC   receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
CC   inhibiting or reducing growth factor mediated cell proliferation,
CC   inflammation and/or other disorders. The present sequence is an
CC   oligonucleotide which can be used to design the antisense
CC   oligonucleotides of the present invention (see AAF45151 and AAF45153-
CC   F45161). The method is useful for ameliorating the effects of psoriasis,
CC   ichthyosis, pityriasis, ruba, pilaris, serborrhoea, keloids, keratosis,
CC   neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
CC   hyperneovascular condition such as a neovascular condition of the retina,
CC   brain or skin, growth factor-mediated malignancies, other sclerotic
CC   disease, kidney disease, hyperproliferation of the inside of blood
CC   vessels or any other hyperplasia
XX
SQ   Sequence 15 BP; 3 A; 5 C; 1 G; 6 T; 0 U; 0 Other;

  Query Match             54.0%;  Score 10.8;  DB 1;  Length 15;
  Best Local Similarity   85.7%;  Pred. No. 25;
  Matches   12;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          7 GGTCACATGGATGA 20
              | ||| ||||||||
Db         15 GATCAGATGGATGA 2


RESULT 34
ABK32412
ID   ABK32412 standard; DNA; 15 BP.
XX
AC   ABK32412;
XX
DT   23-APR-2002  (first entry)
XX
DE   Human colon cancer SAGE tag #513.
XX
KW   Human; colon cancer; colorectal cancer; pancreatic cancer; SAGE tag;
KW   serial analysis of gene expression; diagnostic; prognostic; probe;
KW   cancer marker; ss.
XX
OS   Homo sapiens.
```

XX
PN US6333152-B1.
XX
PD 25-DEC-2001.
XX
PF 20-MAY-1998; 98US-00081646.
XX
PR 20-MAY-1998; 98US-00081646.
XX
PA (UYJO) UNIV JOHNS HOPKINS.
XX
PI Vogelstein B, Kinzler KW, Zhang L, Zhou W;
XX
DR WPI; 2002-153821/20.
XX
PT New human nucleic acid containing specific SAGE tags, useful as
PT diagnostic markers for cancer, also derived probes.
XX
PS Disclosure; Col 57; 161pp; English.
XX
CC The invention relates to an isolated, purified human nucleic acid (I)
CC that has the same sequence as a mRNA found in humans and is a SAGE
CC (serial analysis of gene expression) tag comprising a single stranded
CC probe containing at least 10 consecutive nucleotides. SAGE tags, are
CC diagnostic and prognostic markers of cancer, especially of the colon and
CC pancreas. ABK31900-ABK32770 represent human colon and pancreatic cancer
CC SAGE tags of the invention
XX
SQ Sequence 15 BP; 3 A; 4 C; 6 G; 2 T; 0 U; 0 Other;

Query Match 54.0%; Score 10.8; DB 1; Length 15;
Best Local Similarity 85.7%; Pred. No. 25;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 CATGGTCACATGGA 17
||||| ||| ||||
Db 1 CATGGCCACGTGGA 14

RESULT 35
ADQ82962/c
ID ADQ82962 standard; DNA; 14 BP.
XX
AC ADQ82962;
XX
DT 07-OCT-2004 (first entry)
XX
DE Extended hairpin tail primer #22 for SNP detection method.
XX
KW ss; primer; single nucleotide polymorphism; SNP; amplification;
KW hairpin primer; alleles; drug resistance.
XX
OS Mycobacterium tuberculosis.
XX
PN WO2004061134-A1.
XX
PD 22-JUL-2004.
XX
PF 24-DEC-2003; 2003WO-US041136.
XX
PR 27-DEC-2002; 2002US-0437165P.
XX
PA (UYNE-) UNIV NEW JERSEY MEDICINE & DENTISTRY.
XX
PI Alland D, Hazbon MH;
XX
DR WPI; 2004-553374/53.
XX
PT Detecting single nucleotide polymorphism (SNP) in an organism, useful for
PT identifying SNPs responsible for drug resistance, comprises amplifying a
PT nucleic acid sequence of an organism using a hairpin shaped primer.
XX
PS Example 1; SEQ ID NO 106; 53pp; English.
XX
CC The invention relates to a method of detecting a single nucleotide
CC polymorphism (SNP) in an organism by amplifying a nucleic acid sequence
CC of an organism using a hairpin shaped primer that discriminates between
CC different alleles by situating its 3' nucleotide at the location of a
CC SNP, and measuring threshold cycle or amplification efficiency or amount
CC of amplified product. A lower amplification efficiency or delayed
CC threshold cycle or a difference in the amount of amplified product is
CC indicative of a mismatch between the primer and the organism and a SNP in
CC the organism. The method is useful for efficiently identifying SNPs
CC responsible for drug resistance of infective organisms. The method and
CC kit are useful for analysing large number of isolates, thus providing a
CC means for comprehensive understanding of the frequency and position of
CC mutations in an organism. This sequence corresponds to an extended
CC hairpin tail primer used in the method of the invention
XX
SQ Sequence 14 BP; 4 A; 3 C; 4 G; 3 T; 0 U; 0 Other;

Query Match 52.0%; Score 10.4; DB 1; Length 14;
Best Local Similarity 91.7%; Pred. No. 25;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 TGGTCACATGGA 17
||||||||||
Db 12 TGGTCACATGCA 1

RESULT 36
ADQ82964/c
ID ADQ82964 standard; DNA; 14 BP.
XX
AC ADQ82964;
XX
DT 07-OCT-2004 (first entry)
XX
DE Extended hairpin tail primer #24 for SNP detection method.
XX
KW ss; primer; single nucleotide polymorphism; SNP; amplification;
KW hairpin primer; alleles; drug resistance.
XX
OS Mycobacterium tuberculosis.
XX
PN WO2004061134-A1.
XX
PD 22-JUL-2004.
XX
PF 24-DEC-2003; 2003WO-US041136.
XX
PR 27-DEC-2002; 2002US-0437165P.
XX
PA (UYNE-) UNIV NEW JERSEY MEDICINE & DENTISTRY.
XX
PI Alland D, Hazbon MH;
XX
DR WPI; 2004-553374/53.
XX
PT Detecting single nucleotide polymorphism (SNP) in an organism, useful for
PT identifying SNPs responsible for drug resistance, comprises amplifying a
PT nucleic acid sequence of an organism using a hairpin shaped primer.
XX
PS Example 1; SEQ ID NO 108; 53pp; English.
XX
CC The invention relates to a method of detecting a single nucleotide
CC polymorphism (SNP) in an organism by amplifying a nucleic acid sequence
CC of an organism using a hairpin shaped primer that discriminates between
CC different alleles by situating its 3' nucleotide at the location of a
CC SNP, and measuring threshold cycle or amplification efficiency or amount
CC of amplified product. A lower amplification efficiency or delayed
CC threshold cycle or a difference in the amount of amplified product is
CC indicative of a mismatch between the primer and the organism and a SNP in
CC the organism. The method is useful for efficiently identifying SNPs
CC responsible for drug resistance of infective organisms. The method and
CC kit are useful for analysing large number of isolates, thus providing a

```
CC   means for comprehensive understanding of the frequency and position of
CC   mutations in an organism. This sequence corresponds to an extended
CC   hairpin tail primer used in the method of the invention
XX
SQ   Sequence 14 BP; 4 A; 3 C; 4 G; 3 T; 0 U; 0 Other;

  Query Match             52.0%;  Score 10.4;  DB 1;  Length 14;
  Best Local Similarity   91.7%;  Pred. No. 25;
  Matches   11;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          6 TGGTCACATGGA 17
              |||||||||| |
Db         12 TGGTCACATGCA 1


RESULT 37
AAT36745/c
ID   AAT36745 standard; DNA; 14 BP.
XX
AC   AAT36745;
XX
DT   22-APR-1997  (first entry)
XX
DE   Antisense oligonucleotide to cdk4 gene.
XX
KW   Antisense; phosphorylation; retinoblastoma; tumour suppressor; ribozyme;
KW   antagonist; kinase; cyclin; cdk4; Rb; ss.
XX
OS   Synthetic.
XX
PN   DE19539130-A1.
XX
PD   29-AUG-1996.
XX
PF   20-OCT-1995;   95DE-01039130.
XX
PR   28-FEB-1995;   95DE-01008734.
XX
PA   (PLAC ) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
XX
PI   Strauss M,  Bartek J,  Lukas J,  Sandig V;
XX
DR   WPI; 1996-394264/40.
XX
PT   Compsn. for treating tumour or other hyperplasias - contg. co-operative
PT   gene, antisense or ribozyme against kinase or cyclin or other inhibitor
PT   of Rb phosphorylation.
XX
PS   Claim 12; Page 4; 7pp; German.
XX
CC   The oligonucleotides AAT36744-50 represent antisense oligonucleotides
CC   targeted to genes encoding proteins that interact with, pref. by
CC   phosphorylating the retinoblastoma (Rb) protein. The oligonucleotides are
CC   used in a novel method of treating tumours by using: (a) tumour
CC   suppressor genes that co-operate with the Rb suppressor, (b) antisense or
CC   ribozymes that are antagonistic to kinases or cyclins, or (c) other
CC   compounds that inhibit Rb phosphorylation. This oligonucleotide is
CC   directed to the cyclin-dependent kinase cdk4 gene
XX
SQ   Sequence 14 BP; 3 A; 6 C; 2 G; 3 T; 0 U; 0 Other;

  Query Match             50.0%;  Score 10;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 29;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 GGTCACATGG 16
              ||||||||||
Db         14 GGTCACATGG 5


RESULT 38
AAH89017/c
ID   AAH89017 standard; DNA; 14 BP.
XX
AC   AAH89017;
XX
DT   09-SEP-2004  (revised)
DT   27-FEB-2002  (first entry)
XX
DE   Human polymorphic oligonucleotide U54701 fragment #18.
XX
KW   Human; single nucleotide polymorphic; SNP; forensic science;
KW   paternity testing; phenotypic trait; genetic mapping; animal breeding;
KW   plant breeding; ds.
XX
OS   Homo sapiens.
OS   Unidentified.
XX
FH   Key             Location/Qualifiers
FT   variation       11
FT                   /*tag=  a
FT                   /standard_name= "single nucleotide polymorphism"
XX
PN   WO200134840-A2.
XX
PD   17-MAY-2001.
XX
PF   10-NOV-2000; 2000WO-US030766.
XX
PR   10-NOV-1999;   99US-0164596P.
XX
PA   (GLAX ) GLAXO GROUP LTD.
PA   (AFFY-) AFFYMETRIX INC.
XX
PI   Au K,  Chen J,  Patil N,  Thomas D;
XX
DR   WPI; 2001-335945/35.
XX
PT   New polymorphic sites derived from the human genome are useful to
PT   determine sites correlating with phenotypic traits, particularly disease,
PT   and also in forensics and paternity testing.
XX
PS   Claim 69; Page 11; 43pp; English.
XX
CC   The present invention relates to human oligonucleotides comprising a
CC   single nucleotide polymorphic site (SNP: AAH88797-AAH89219). The present
CC   sequence is one such oligonucleotide. The oligonucleotides can be used in
CC   forensics, paternity testing, correlation of polymorphisms with
CC   phenotypic traits, genetic mapping of phenotypic traits and marker
CC   assisted breeding of animals and crop plants
CC
CC   Revised record issued on 09-SEP-2004 : Correction to Feature Table Key
XX
SQ   Sequence 14 BP; 2 A; 5 C; 2 G; 5 T; 0 U; 0 Other;

  Query Match             50.0%;  Score 10;  DB 1;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 29;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          8 GTCACATGGA 17
              ||||||||||
Db         10 GTCACATGGA 1


RESULT 39
ABH45285/c
ID   ABH45285 standard; DNA; 13 BP.
XX
AC   ABH45285;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide SEQ ID NO 245262 for detecting SNP TSC0059887.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
```

KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 245262; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 13 BP; 4 A; 5 C; 1 G; 3 T; 0 U; 0 Other;

Query Match 49.0%; Score 9.8; DB 1; Length 13;
Best Local Similarity 84.6%; Pred. No. 27;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 6 TGGTCACATGGAT 18
|||| || |||||
Db 13 TGGTAACGTGGAT 1

RESULT 40
ABH45284
ID ABH45284 standard; DNA; 13 BP.
XX
AC ABH45284;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 245261 for detecting SNP TSC0059887.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 245261; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 13 BP; 3 A; 1 C; 5 G; 4 T; 0 U; 0 Other;

Query Match 49.0%; Score 9.8; DB 1; Length 13;
Best Local Similarity 84.6%; Pred. No. 27;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 6 TGGTCACATGGAT 18
|||| || |||||
Db 1 TGGTAACGTGGAT 13

RESULT 41
ABH28185/c
ID ABH28185 standard; DNA; 13 BP.
XX
AC ABH28185;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 228162 for detecting SNP TSC0055641.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 228162; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)

```
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 13 BP; 4 A; 5 C; 1 G; 3 T; 0 U; 0 Other;

  Query Match             49.0%;  Score 9.8;  DB 1;  Length 13;
  Best Local Similarity   84.6%;  Pred. No. 27;
  Matches   11;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          8 GTCACATGGATGA 20
              || || |||||||
Db         13 GTTACGTGGATGA 1


RESULT 42
ABH28184
ID   ABH28184 standard; DNA; 13 BP.
XX
AC   ABH28184;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide SEQ ID NO 228161 for detecting SNP TSC0055641.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 228161; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 13 BP; 3 A; 1 C; 5 G; 4 T; 0 U; 0 Other;

  Query Match             49.0%;  Score 9.8;  DB 1;  Length 13;
  Best Local Similarity   84.6%;  Pred. No. 27;
  Matches   11;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          8 GTCACATGGATGA 20
              || || |||||||
Db          1 GTTACGTGGATGA 13


RESULT 43
AAN70553/c
ID   AAN70553 standard; DNA; 14 BP.
XX
AC   AAN70553;
XX
DT   25-MAR-2003  (revised)
DT   29-APR-1991  (first entry)
XX
DE   Sequence of probe which corresponds to the AA sequence W-N-Y-L-D (515-
DE   519) of human tissue plasminogen activator (TPA).
XX
KW   Thrombolytic; enzyme; protease; ss.
XX
OS   Homo sapiens.
XX
PN   EP211260-A.
XX
PD   25-FEB-1987.
XX
PF   09-JUL-1986;   86EP-00109385.
XX
PR   10-JUL-1985;   85JP-00152810.
PR   31-JAN-1986;   86JP-00020469.
PR   26-APR-1986;   86JP-00097481.
XX
PA   (KANF ) KANEGAFUCHI KAGAKU KOGYO KK.
PA   (KANF-) KANEGAFUCHI.
XX
PI   Kakutani T,  Matsumoto K,  Yahara H,  Maruyama H,  Kawaharada H;
PI   Watanabe K;
XX
DR   WPI; 1987-051507/08.
XX
PT   New chromosomal DNA coding for human tissue plasminogen activator -
PT   useful in expression vectors for high yield prodn. of activator by large
PT   scale suspension culture.
XX
PS   Example; p29; 70pp; English.
XX
CC   The probe is used in an example to exemplify the cloning of TPA gene.
CC   (Updated on 25-MAR-2003 to correct PA field.)
XX
SQ   Sequence 14 BP; 4 A; 4 C; 4 G; 2 T; 0 U; 0 Other;

  Query Match             49.0%;  Score 9.8;  DB 1;  Length 14;
  Best Local Similarity   84.6%;  Pred. No. 31;
  Matches   11;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          3 TCATGGTCACATG 15
              ||| |||| ||||
Db         14 TCACGGTCGCATG 2


RESULT 44
AAX19072/c
ID   AAX19072 standard; DNA; 13 BP.
XX
AC   AAX19072;
XX
DT   13-MAY-1999  (first entry)
XX
DE   Human PPAR-gamma-3-E-box SEQ ID NO:41.
XX
```

KW Human; peroxisome proliferator activated receptor gamma; PPAR-gamma;
KW regulatory sequence; promoter; obesity; anorexia; lipoma; cachexia;
KW lipodystrophy; liposarcoma; human immunodeficiency virus; HIV;
KW insulin resistance; non-insulin-dependent diabetes mellitus;
KW polycystic ovary syndrome; gastrointestinal tract; Crohn's disease;
KW inflammatory bowel disease; ulcerative colitis; bowel cancer; ss.
XX
OS Homo sapiens.
XX
PN WO9905161-A1.
XX
PD 04-FEB-1999.
XX
PF 24-JUL-1998; 98WO-US015411.
XX
PR 25-JUL-1997; 97US-0053692P.
XX
PA (LIGA-) LIGAND PHARM INC.
PA (INSP) INST PASTEUR.
XX
PI Briggs MR, Saladin RS, Auwerx J, Fajas L;
XX
DR WPI; 1999-142844/12.
XX
PT Newly isolated nucleic acid comprising a control region of a human
PT peroxisome proliferator activated receptor (PPAR) gamma gene - useful for
PT identifying modulators that are useful in treating diseases associated
PT with abnormal levels of human PPAR-gamma gene expression.
XX
PS Disclosure; Page 91; 102pp; English.
XX
CC The present invention describes an isolated, purified or enriched nucleic
CC acid comprising a control region of a human peroxisome proliferator
CC activated receptor gamma (PPAR-gamma) gene. The nucleic acids are useful
CC for screening for agents capable of modulating the expression of a human
CC PPAR-gamma gene. These agents (modulators) form pharmaceutical
CC compositions that are useful for treating diseases associated with
CC high/low levels of human PPAR-gamma gene expression. The diseases include
CC obesity, anorexia, cachexia, lipodystrophy, lipomas, liposarcomas,
CC abnormalities associated with anti-human immunodeficiency virus (HIV)
CC treatment, insulin resistance, non-insulin-dependent diabetes mellitus
CC (NIDDM), polycystic ovary syndrome, diseases of the gastrointestinal (GI)
CC tract, inflammatory bowel disease, Crohn's disease, ulcerative colitis
CC and bowel cancer. The nucleic acids are useful for studying the role of
CC the PPAR-gamma gene in various diseases and disorders. The structure of
CC PPAR-gamma enables genetic studies of PPAR- gamma mutations in humans,
CC and evaluation of its role in disorders like insulin resistance, NIDDM,
CC and diseases associated with altered adipose tissue function, like
CC obesity and lipodystrophic syndromes. The nucleic acids are also useful
CC for gene therapy and the production of transgenic animals, which are
CC useful in screening assays. The control regions of the nucleic acids
CC enable screening for modulators of the human PPAR-gamma gene, which are
CC useful in designing drugs for treating disorders or diseases associated
CC with the level of PPAR-gamma gene expression. The present sequence
CC represents the human PPAR-gamma-3-E-box
XX
SQ Sequence 13 BP; 4 A; 2 C; 2 G; 5 T; 0 U; 0 Other;

Query Match 47.0%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 31;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 8 GTCACATGGAT 18
||||||||| ||
Db 11 GTCACATGAAT 1

RESULT 45
ADZ24722
ID ADZ24722 standard; DNA; 13 BP.
XX
AC ADZ24722;
XX
DT 16-JUN-2005 (first entry)
XX
DE Human SNP detection related oligonucelotide #1689.
XX
KW ss; haplotype mapping; SNP detection; tumor; cytostatic; neoplasm;
KW immune disorder; cardiovascular disease; metabolic disorder;
KW respiratory disease; musculoskeletal disease; renal disease;
KW nephrotropic; endocrine disease; genitourinary disease.
XX
OS Homo sapiens.
XX
PN WO2005030952-A1.
XX
PD 07-APR-2005.
XX
PF 30-SEP-2004; 2004WO-JP014784.
XX
PR 30-SEP-2003; 2003JP-00342519.
PR 28-MAY-2004; 2004JP-00158717.
XX
PA (RIKE) RIKEN KK.
PA (STAG-) STAGEN CO LTD.
PA (SEKI/) SEKINE A.
PA (IIDA/) IIDA A.
PA (SAIT/) SAITO S.
XX
PI Sekine A, Iida A, Saito S, Nakamura Y, Kamatani N;
XX
DR WPI; 2005-305936/31.
XX
PT Analyzing haplotype, by detecting polymorphism in drug-related genes,
PT electing common polymorphism (CP), building haplotype block using CP,
PT specifying CP within block, specifying tag polymorphism from CP within
PT block.
XX
PS Disclosure; SEQ ID NO 1689; 1290pp; Japanese.
XX
CC The invention relates to a method of analyzing haplotype, by detecting
CC gene polymorphism in drug-related genes such as aryl acetylamide
CC deacetylase, arylalkylamine N-acetyl transferase or ATP-binding cassette,
CC sub-family A (ABC1), member 1. The method is useful for analyzing
CC haplotype. The method is useful for estimating the sensitivity or disease
CC of a medicine or a foreign material, for selecting medicine for
CC preventing or treating diseases, for determining appropriate dosage of
CC medicine for preventing or treating a disease, for analyzing a drug
CC interaction, and for determining the related polymorphism relative to the
CC sensitivity of the medicine, foreign material or disease. The diseases
CC include malignant tumor, immune disorder circulatory disease, metabolic
CC disease, kidney disease, respiratory disease and muscle associated
CC disease. The method enables analysis of the individual differences
CC related to the sensitivity of a medicine, using a haplotype, without
CC using each single nucleotide polymorphism. The present sequence
CC represents a human SNP detection related oligonucelotide.
XX
SQ Sequence 13 BP; 2 A; 5 C; 3 G; 3 T; 0 U; 0 Other;

Query Match 47.0%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 31;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCTCATGGTCA 11
||||||| |||
Db 2 CCTCATGCTCA 12

RESULT 46
AED86939
ID AED86939 standard; DNA; 13 BP.
XX
AC AED86939;
XX
DT 12-JAN-2006 (first entry)
XX

```
DE   Polyamide-binding target oligonucleotide I, SEQ ID NO:12.
XX
KW   Gene expression; transcription factor inhibitor; DNA footprinting; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_binding    1. .13
FT                   /*tag=  a
FT                   /bound_moiety= "Bases 13-1 of SEQ ID NO:13"
FT   misc_binding    7. .10
FT                   /*tag=  b
FT                   /bound_moiety= "Imidazole- and pyrrole-containing
FT                   polyamide chain"
FT                   /note= "Polyamide chain binds to the minor groove of the
FT                   dsDNA in a sequence-specific manner"
XX
PN   US6958240-B1.
XX
PD   25-OCT-2005.
XX
PF   12-AUG-1999;   99US-00374704.
XX
PR   26-FEB-1996;   96US-00607078.
PR   20-FEB-1997;   97WO-US003332.
PR   08-APR-1997;   97US-0043444P.
PR   16-APR-1997;   97US-0042022P.
PR   21-APR-1997;   97US-00837524.
PR   08-MAY-1997;   97US-00853522.
XX
PA   (CALY ) CALIFORNIA INST OF TECHNOLOGY.
XX
PI   Baird EE,  Dervan PB;
XX
DR   WPI; 2005-807194/82.
XX
PT   Novel polyamides comprising amino acids having N-methylpyrrole, 3-hydroxy
PT   -N-methylpyrrole and/or N-methylimidazole groups and positive patches
PT   having rigid groups adjacent to positively charged groups, useful for
PT   inhibiting gene expression.
XX
PS   Example 4; SEQ ID NO 12; 43pp; English.
XX
CC   The invention relates to a polyamide molecule which specifically binds to
CC   a predetermined site in the minor groove of a double-stranded DNA
CC   molecule in a sequence-specific manner and which contains an alpha-amino
CC   acid domain (termed the "positive patch") which contacts nucleotides in
CC   the major groove and thus inhibits the activity of major groove DNA-
CC   binding proteins. The polyamide molecule comprises one or more amino
CC   acids containing a N-methylpyrrole, 3-hydroxy-N-methylpyrrole and/or N-
CC   methylimidazole group, where one or more of these amino acid(s) are not
CC   alpha-amino acids, and a positive patch consisting of a 2 amino acid
CC   rigid group adjacent to a positively charged group (such as a positively
CC   charged amino acid). The polyamides of the invention inhibit gene
CC   expression by displacing or preventing the function of DNA-binding
CC   proteins such as transcription factors. The invention also relates to a
CC   method of inhibiting gene expression by contacting a regulatory sequence
CC   of a gene with a polyamide of the invention. The polyamide of the
CC   invention is useful for inhibiting the binding and activity of DNA-
CC   binding proteins, thus inhibiting gene expression. Sequences AED86939-
CC   AED86940 represent the two strands of a double-stranded oligonucleotide
CC   which is capable of being bound by a polyamide of the invention. This
CC   oligonucleotide was used in DNase I footprinting in an example of the
CC   invention to determine the optimum positive patch peptide sequence for
CC   inhibition of protein binding.
XX
SQ   Sequence 13 BP; 5 A; 2 C; 2 G; 4 T; 0 U; 0 Other;

  Query Match             47.0%;  Score 9.4;  DB 1;  Length 13;
  Best Local Similarity   90.9%;  Pred. No. 31;
  Matches   10;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 TCATGGTCACA 13
              |||||||||| |
Db          3 TCATGGTCATA 13


RESULT 47
AED86940/c
ID   AED86940 standard; DNA; 13 BP.
XX
AC   AED86940;
XX
DT   12-JAN-2006  (first entry)
XX
DE   Polyamide-binding target oligonucleotide I, SEQ ID NO:13.
XX
KW   Gene expression; transcription factor inhibitor; DNA footprinting; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_binding    1. .13
FT                   /*tag=  a
FT                   /bound_moiety= "Bases 13-1 of SEQ ID NO:12"
FT   misc_binding    4. .13
FT                   /*tag=  d
FT                   /bound_moiety= "Imidazole- and pyrrole-containing
FT                   polyamide chain with Arg-Pro-Arg-Arg-Arg-Arg positive
FT                   patch"
FT                   /note= "Polyamide chain binds to the minor groove of the
FT                   dsDNA in a sequence-specific manner"
FT   misc_binding    4. .10
FT                   /*tag=  c
FT                   /bound_moiety= "Imidazole- and pyrrole-containing
FT                   polyamide chain with Arg-Pro-Arg positive patch"
FT                   /note= "Polyamide chain binds to the minor groove of the
FT                   dsDNA in a sequence-specific manner"
FT   misc_binding    4. .9
FT                   /*tag=  b
FT                   /bound_moiety= "Imidazole- and pyrrole-containing
FT                   polyamide chain"
FT                   /note= "Polyamide chain binds to the minor groove of the
FT                   dsDNA in a sequence-specific manner"
XX
PN   US6958240-B1.
XX
PD   25-OCT-2005.
XX
PF   12-AUG-1999;   99US-00374704.
XX
PR   26-FEB-1996;   96US-00607078.
PR   20-FEB-1997;   97WO-US003332.
PR   08-APR-1997;   97US-0043444P.
PR   16-APR-1997;   97US-0042022P.
PR   21-APR-1997;   97US-00837524.
PR   08-MAY-1997;   97US-00853522.
XX
PA   (CALY ) CALIFORNIA INST OF TECHNOLOGY.
XX
PI   Baird EE,  Dervan PB;
XX
DR   WPI; 2005-807194/82.
XX
PT   Novel polyamides comprising amino acids having N-methylpyrrole, 3-hydroxy
PT   -N-methylpyrrole and/or N-methylimidazole groups and positive patches
PT   having rigid groups adjacent to positively charged groups, useful for
PT   inhibiting gene expression.
XX
PS   Example 4; SEQ ID NO 13; 43pp; English.
XX
CC   The invention relates to a polyamide molecule which specifically binds to
CC   a predetermined site in the minor groove of a double-stranded DNA
CC   molecule in a sequence-specific manner and which contains an alpha-amino
CC   acid domain (termed the "positive patch") which contacts nucleotides in
CC   the major groove and thus inhibits the activity of major groove DNA-
```

```
CC   binding proteins. The polyamide molecule comprises one or more amino
CC   acids containing a N-methylpyrrole, 3-hydroxy-N-methylpyrrole and/or N-
CC   methylimidazole group, where one or more of these amino acid(s) are not
CC   alpha-amino acids, and a positive patch consisting of a 2 amino acid
CC   rigid group adjacent to a positively charged group (such as a positively
CC   charged amino acid). The polyamides of the invention inhibit gene
CC   expression by displacing or preventing the function of DNA-binding
CC   proteins such as transcription factors. The invention also relates to a
CC   method of inhibiting gene expression by contacting a regulatory sequence
CC   of a gene with a polyamide of the invention. The polyamide of the
CC   invention is useful for inhibiting the binding and activity of DNA-
CC   binding proteins, thus inhibiting gene expression. Sequences AED86939-
CC   AED86940 represent the two strands of a double-stranded oligonucleotide
CC   which is capable of being bound by a polyamide of the invention. This
CC   oligonucleotide was used in DNase I footprinting in an example of the
CC   invention to determine the optimum positive patch peptide sequence for
CC   inhibition of protein binding.
XX
SQ   Sequence 13 BP; 4 A; 2 C; 2 G; 5 T; 0 U; 0 Other;

  Query Match             47.0%;  Score 9.4;  DB 1;  Length 13;
  Best Local Similarity   90.9%;  Pred. No. 31;
  Matches   10;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 TCATGGTCACA 13
              ||||||||| |
Db         11 TCATGGTCATA 1


RESULT 48
AAQ88597/c
ID   AAQ88597 standard; DNA; 12 BP.
XX
AC   AAQ88597;
XX
DT   21-DEC-1995  (first entry)
XX
DE   Human mitochondrial D-loop region DNA probe 6-10.
XX
KW   Tiling strategy; immobilised nucleic acid probe array; mitochondrial DNA;
KW   D-loop region; biological chip; hybridisation fingerprint;
KW   interrogation position; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   12
FT                   /*tag=  a
FT                   /note= "3'-end of probe is covalently attached to chip
FT                   surface"
XX
PN   WO9511995-A1.
XX
PD   04-MAY-1995.
XX
PF   26-OCT-1994;   94WO-US012305.
XX
PR   26-OCT-1993;   93US-00143312.
PR   02-AUG-1994;   94US-00284064.
XX
PA   (AFFY-) AFFYMAX TECHNOLOGIES NV.
XX
PI   Chee M,  Cronin MT,  Fodor SP,  Gingeras TR,  Huang XC,  Hubbell EA;
PI   Lipshutz RJ,  Lobban PE,  Miyada CG,  Morris MS,  Shah N,  Sheldon EL;
XX
DR   WPI; 1995-178887/23.
XX
PT   New arrays of oligo:nucleotide probes - used for comparing known
PT   sequences with variants for detection of mutation(s) and sequencing.
XX
PS   Disclosure; Page 108; 223pp; English.
XX
CC   A DNA chip was prepared for analysing sequences contained in a 1.3kb
CC   fragment of human mitochondrial DNA from the D-loop region, the most
CC   polymorphic region of human mitochondrial DNA. The chip comprised a set
CC   of 268 overlapping oligonucleotide probes (see AAQ88421-Q88684) of
CC   varying length (9-14 nucleotides) with varying overlaps arranged in a 1cm
CC   x 1cm array. Each position in the sequence was represented by at least
CC   one probe (usually 2 or more). DNA was amplified from six human donors
CC   and then transcribed to give the 1.3kb RNA transcripts which were
CC   fragmented and hybridised to the chip. For each individual, a unique
CC   hybridisation fingerprint was produced on the chip; all differences could
CC   be correlated with differences in the cloned genomic DNA sequence
XX
SQ   Sequence 12 BP; 2 A; 3 C; 4 G; 3 T; 0 U; 0 Other;

  Query Match             45.0%;  Score 9;  DB 1;  Length 12;
  Best Local Similarity   100.0%;  Pred. No. 30;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          12 CATGGATGA 20
               |||||||||
Db          11 CATGGATGA 3


RESULT 49
AAV32269
ID   AAV32269 standard; DNA; 12 BP.
XX
AC   AAV32269;
XX
DT   18-AUG-1998  (first entry)
XX
DE   Random primed reverse transcription PCR primer 114.
XX
KW   RT-PCR; primer; amplification; reverse transcription; RNA fingerprinting;
KW   differential gene expression; ss.
XX
OS   Synthetic.
XX
PN   WO9813521-A1.
XX
PD   02-APR-1998.
XX
PF   26-SEP-1997;   97WO-EP005290.
XX
PR   27-SEP-1996;   96GB-00020216.
XX
PA   (SANR-) FOND CENT SAN RAFFAELE DEL MONTE TABOR.
XX
PI   Consalez G,  Fesce R;
XX
DR   WPI; 1998-230725/20.
XX
PT   Differential screening of gene expression by reverse transcription
PT   polymerase chain reaction - uses random priming with primers selected for
PT   high efficiency and selectivity by computer screening of database(s).
XX
PS   Claim 9; Page 24; 37pp; English.
XX
CC   The invention provides a method for the differential screening of gene
CC   expression by random primed reverse transcription PCR (RT-PCR). The
CC   primer sequences are generated by stimulating PCR reactions on non-
CC   redundant mammalian nucleotide sequence databank entries containing at
CC   least 1,000 bp of coding region. The primers selected, such as the
CC   present one, had to meet various criteria such as having an efficiency
CC   index between 2-10, having a selectivity index higher than 1, being 12 bp
CC   long i.e. 8 C or G and 4 T or A, and each primer differed from the others
CC   in at least 5 of the 8 bases at the 3'-end. The invention claims the
CC   selected primers make it possible to use internally primed, PCR-based RNA
CC   fingerprinting for simple, exhaustive and systematic analysis of
CC   differential gene expression as an advantageous alternative to
CC   differential display. The method can also be useful for isolating new
CC   coding sequences and to compare known and new genes
XX
SQ   Sequence 12 BP; 1 A; 3 C; 4 G; 3 T; 0 U; 1 Other;
```

```
  Query Match             45.0%;  Score 9;  DB 1;  Length 12;
  Best Local Similarity   81.8%;  Pred. No. 30;
  Matches    9;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          6 TGGTCACATGG 16
              ||||||| ||:
Db          2 TGGTCACGTGS 12


RESULT 50
AAH23540/c
ID   AAH23540 standard; DNA; 12 BP.
XX
AC   AAH23540;
XX
DT   03-AUG-2001  (first entry)
XX
DE   Antibacterial peptide nucleic acid oligonucleotide #49.
XX
KW   Peptide nucleic acid; PNA; antimicrobial; antibiotic; cationic peptide;
KW   antisense; disinfectant; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base    1
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "linked to AAB99988 by 8-amino-3,6-dioxaoctanoic
FT                   acid"
XX
PN   WO200127262-A1.
XX
PD   19-APR-2001.
XX
PF   13-OCT-2000; 2000WO-DK000581.
XX
PR   13-OCT-1999;   99DK-00001468.
PR   15-OCT-1999;   99US-0159683P.
XX
PA   (PANT-) PANTHECO AS.
XX
PI   Nielsen PE,  Schou C,  Wissenbach M;
XX
DR   WPI; 2001-290722/30.
XX
PT   Identifying target genes in a microorganism (e.g. Escherichia coli) as a
PT   basis for anti-infective treatment comprises selecting potential targets
PT   known to be present and obtaining complementary (antisense) peptide
PT   nucleic acid sequences.
XX
PS   Example 3; Page 35; 57pp; English.
XX
CC   The present invention describes a method of identifying target genes, for
CC   use in anti-infective treatments, in a microorganism, involving obtaining
CC   antisense peptide nucleic acid (PNA) sequences for potential target
CC   genes, mixing them with the organism in culture and comparing the growth
CC   in the presence and absence of the antisense PNA sequence, where a useful
CC   target gene is one which results in decreased growth when blocked by the
CC   antisense sequence. Antisense oligonucleotides are linked to cationic
CC   peptides via a linking group for use as antimicrobial compounds,
CC   particularly as antibiotics. The present sequence is an oligonucleotide
CC   useful as the antisense portion of a PNA in the present invention
XX
SQ   Sequence 12 BP; 4 A; 5 C; 2 G; 1 T; 0 U; 0 Other;

  Query Match             44.0%;  Score 8.8;  DB 1;  Length 12;
  Best Local Similarity   83.3%;  Pred. No. 33;
  Matches   10;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          7 GGTCACATGGAT 18
              |||||| ||| |
Db         12 GGTCACGTGGTT 1


RESULT 51
ABH82120
ID   ABH82120 standard; DNA; 12 BP.
XX
AC   ABH82120;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide primer SEQ ID NO 282113 for detecting SNP TSC0010416.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 282113; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 12 BP; 3 A; 0 C; 4 G; 5 T; 0 U; 0 Other;

  Query Match             44.0%;  Score 8.8;  DB 1;  Length 12;
  Best Local Similarity   83.3%;  Pred. No. 33;
  Matches   10;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          6 TGGTCACATGGA 17
              |||| | |||||
Db          1 TGGTTATATGGA 12


RESULT 52
ABI08296
ID   ABI08296 standard; DNA; 12 BP.
XX
AC   ABI08296;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide primer SEQ ID NO 308269 for detecting SNP TSC0022931.
XX
```

```
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 308269; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 12 BP; 2 A; 7 C; 0 G; 3 T; 0 U; 0 Other;

  Query Match             44.0%;  Score 8.8;  DB 1;  Length 12;
  Best Local Similarity   83.3%;  Pred. No. 33;
  Matches   10;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 CCTCATGGTCAC 12
              ||||||  ||||
Db          1 CCTCATCCTCAC 12


RESULT 53
ADW11578
ID   ADW11578 standard; RNA; 12 BP.
XX
AC   ADW11578;
XX
DT   24-MAR-2005  (first entry)
XX
DE   siRNA production-related p4 box RNA SeqID15.
XX
KW   short interfering RNA; siRNA; RNA interference; ribozyme; ss.
XX
OS   Unidentified.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_binding    1. .4
FT                   /*tag=  b
FT                   /bound_moiety= "Itself"
FT                   /note= "Binds nucleotides 12-9 of itself"
FT   misc_binding    9. .12
FT                   /*tag=  b
FT                   /bound_moiety= "Itself"
FT                   /note= "Binds nucleotides 4-1 of itself"
XX
PN   WO2005001039-A2.
XX
PD   06-JAN-2005.
XX
PF   28-MAY-2004; 2004WO-US017034.
XX
PR   29-MAY-2003; 2003US-0474001P.
XX
PA   (UYCR-) UNIV CREIGHTON.
XX
PI   Soukup GA,  Kertsburg A;
XX
DR   WPI; 2005-075534/08.
XX
PT   Producing a small, interfering RNA (siRNA) by providing a first or second
PT   RNA construct comprising a first or second ribozyme operably linked to a
PT   sense or an antisense strand, respectively of an siRNA.
XX
PS   Example 1; SEQ ID NO 15; 43pp; English.
XX
CC   This invention relates to a novel method of producing a small interfering
CC   RNA (siRNA). The method comprises providing a first RNA construct
CC   comprising a first ribozyme operably linked to a sense and antisense
CC   strand of an siRNA and placing the first and second RNA constructs under
CC   conditions where the first and second ribozyme catalyze the cleavage of
CC   the sense and antisense strands of the siRNA from the first and second
CC   RNA constructs. The present sequence is that of a p4 box RNA which was
CC   used during the exemplification of the method of the invention.
XX
SQ   Sequence 12 BP; 5 A; 2 C; 3 G; 0 T; 2 U; 0 Other;

  Query Match             44.0%;  Score 8.8;  DB 1;  Length 12;
  Best Local Similarity   66.7%;  Pred. No. 33;
  Matches    8;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          4 CATGGTCACATG 15
              ||:||  |||:|
Db          1 CAUGGAAACAUG 12


RESULT 54
AAQ24034
ID   AAQ24034 standard; DNA; 12 BP.
XX
AC   AAQ24034;
XX
DT   25-MAR-2003  (revised)
DT   21-SEP-1992  (first entry)
XX
DE   Herpesvirus inhibiting antisense oligonucleotide.
XX
KW   HSV; treatment; diagnosis; HSV-1; HSV-2; varicella zoster;
KW   Epstein-Barr virus; cytomegalovirus; CMV; HIV; AIDS.
XX
OS   Synthetic.
XX
PN   WO9205284-A.
XX
PD   02-APR-1992.
XX
PF   18-SEP-1991;   91WO-US006646.
XX
PR   21-SEP-1990;   90US-00586185.
XX
PA   (UYMA-) UNIV MARYLAND BALTIMORE.
PA   (UYJO ) UNIV JOHNS HOPKINS.
XX
PI   Aurelian L,  Tso P;
XX
DR   WPI; 1992-132145/16.
XX
```

```
PT   New anti:sense oligo:nucleotide(s) for inhibiting HSV - also used for
PT   diagnosis and for inhibiting HIV activation by herpes virus.
XX
PS   Claim 1; Page 38; 77pp; English.
XX
CC   The sequence is that of an antisense oligonucleotide which can be used
CC   for inhibiting growth or replication of herpesviruses. It corresponds to
CC   an antisense sequence of a herpesvirus site, pref. in a gene that is
CC   essential for synthesising nucleic acids e.g. the immediate early genes
CC   or Vmw65. It can be prepd. by solid phase triester or phosphor- amidite
CC   chemistry or by recombinant DNA techniques. It can be used for treating
CC   infection by herpesviruses, e.g. herpes simplex type 1 (HSV-1) and type 2
CC   (HSV-2), varicella zoster (VSV), Epstein-Barr (EBV), cytomegalovirus
CC   (CMV), human herpesvirus 6 (HHV-6) and 7 (HHV-7). In addition, the
CC   inhibition of herpesvirus growth or replication may indirectly forestall
CC   the progression of events from HIV exposure to the clinical manifestation
CC   of AIDS. It may also be useful in the detection, diagnosis and
CC   manipulation of herpes virus. See also AAQ23764-Q23788 and AAQ24014-
CC   Q24044. (Updated on 25-MAR-2003 to correct PA field.)
XX
SQ   Sequence 12 BP; 5 A; 3 C; 2 G; 2 T; 0 U; 0 Other;

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 12;
  Best Local Similarity   90.0%;  Pred. No. 37;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          4 CATGGTCACA 13
              |||||| |||
Db          2 CATGGTAACA 11


RESULT 55
AAQ30497/c
ID   AAQ30497 standard; DNA; 12 BP.
XX
AC   AAQ30497;
XX
DT   25-MAR-2003  (revised)
DT   19-MAR-1993  (first entry)
XX
DE   Adenovirus major late transcription factor element under control of TCRE.
XX
KW   Transcriptional control recognition element; decoy; cellular RNA;
KW   promoter; hormone receptor element; viral; liver; tissue; viral;
KW   proliferation; linker; NF-1; ss.
XX
OS   Synthetic.
XX
PN   WO9218522-A1.
XX
PD   29-OCT-1992.
XX
PF   17-APR-1992;   92WO-US003205.
XX
PR   18-APR-1991;   91US-00687337.
XX
PA   (SALK ) SALK INST BIOLOGICAL STUDIES.
XX
PI   Chu BC,  Orgel L;
XX
DR   WPI; 1992-382035/46.
XX
PT   New oligo-nucleotide(s) contg. transcription control recognition element
PT   - stabilised by covalent bonding of two DNA strands, act as decoys for
PT   regulatory protein to modulate specific RNA.
XX
PS   Disclosure; Page 6; 41pp; English.
XX
CC   Transcriptional control recognition element recognition sequences may be
CC   recognised by control proteins and are involved in either enhancing or
CC   repressing transcription of associated sequences. TCR sequences include
CC   promoter elements, hormone receptor elements, viral, cellular, liver or
CC   tissue elements, etc. The sequence represents an exemplary viral and
CC   cellular element, the adenovirus major late transcription factor. A
CC   typical application of the TCRE recognising oligonucleotides is
CC   inhibition of viral proliferation. See also AAQ30472-518. (Updated on 25-
CC   MAR-2003 to correct PN field.)
XX
SQ   Sequence 12 BP; 2 A; 5 C; 4 G; 1 T; 0 U; 0 Other;

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 12;
  Best Local Similarity   90.0%;  Pred. No. 37;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          7 GGTCACATGG 16
              |||||| |||
Db         12 GGTCACGTGG 3


RESULT 56
AAQ52946/c
ID   AAQ52946 standard; RNA; 12 BP.
XX
AC   AAQ52946;
XX
DT   25-MAR-2003  (revised)
DT   26-MAY-1994  (first entry)
XX
DE   Herpes simplex virus target sequence 24.
XX
KW   RNA; enzyme; enzymatic RNA molecule; ERM; cleave; RNA; mRNA; HnRNA;
KW   picornavirus; HIV; immunodeficiency virus; hepatitis B virus; HBV;
KW   papilloma virus; HPV; Epstein-Barr virus; EBV; TCLV;
KW   T-cell leukaemia virus; hepatitis C virus; HCV; cytomegalovirus;
KW   influenza virus; HSV; herpes simplex virus; vector; immune response;
KW   antibody; ribozyme; viral RNA; treatment; ss.
XX
OS   Synthetic.
XX
PN   WO9323569-A1.
XX
PD   25-NOV-1993.
XX
PF   29-APR-1993;   93WO-US004020.
XX
PR   11-MAY-1992;   92US-00882689.
PR   14-MAY-1992;   92US-00882712.
PR   14-MAY-1992;   92US-00882713.
PR   14-MAY-1992;   92US-00882714.
PR   14-MAY-1992;   92US-00882823.
PR   14-MAY-1992;   92US-00882824.
PR   14-MAY-1992;   92US-00882886.
PR   14-MAY-1992;   92US-00882888.
PR   14-MAY-1992;   92US-00882889.
PR   14-MAY-1992;   92US-00882921.
PR   14-MAY-1992;   92US-00882922.
PR   14-MAY-1992;   92US-00883823.
PR   14-MAY-1992;   92US-00883849.
PR   14-MAY-1992;   92US-00884073.
PR   14-MAY-1992;   92US-00884074.
PR   14-MAY-1992;   92US-00884333.
PR   14-MAY-1992;   92US-00884422.
PR   14-MAY-1992;   92US-00884431.
PR   14-MAY-1992;   92US-00884436.
PR   14-MAY-1992;   92US-00884521.
PR   31-JUL-1992;   92US-00923738.
PR   26-AUG-1992;   92US-00935854.
PR   26-AUG-1992;   92US-00936086.
PR   18-SEP-1992;   92US-00948359.
PR   15-OCT-1992;   92US-00963322.
PR   07-DEC-1992;   92US-00987129.
PR   07-DEC-1992;   92US-00987130.
PR   07-DEC-1992;   92US-00987133.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
```

PI Draper KG, Dudycz LW, Mcswiggen JA, Macejak DG, Holecek JJ;
PI Mamone JA;
XX
DR WPI; 1993-386599/48.
XX
PT Enzymatic RNA molecules - used to inhibit viral replication, infection
PT and gene expression.
XX
PS Claim 5; Fig 15; 287pp; English.
XX
CC The sequences (AAQ52923-Q53037) are pref. herpes simplex virus target
CC sequences for enzymatic RNA molecules. The RNA molecules are
CC complementary to a substrate binding region in the specified gene target.
CC They also have enzymatic activity, in that they specifically cleave RNA
CC in the target. The ERMs interfere with viral replication and therefore
CC have anti-viral properties. They can be used to attenuate viruses to be
CC used in vaccines. (Updated on 25-MAR-2003 to correct PN field.) (Updated
CC on 25-MAR-2003 to correct PR field.) (Updated on 25-MAR-2003 to correct
CC PI field.)
XX
SQ Sequence 12 BP; 2 A; 4 C; 4 G; 0 T; 2 U; 0 Other;

Query Match 42.0%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 37;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 TCATGGTCAC 12
||||||.|||
Db 12 TCATGGCCAC 3

RESULT 57
AAZ59958/c
ID AAZ59958 standard; DNA; 12 BP.
XX
AC AAZ59958;
XX
DT 19-APR-2000 (first entry)
XX
DE Adenovirus Ad5 major late promoter (MLP) upstream promoter element (UPE).
XX
KW Major late promoter; MLP; mutation; upstream promoter element; UPE;
KW recombinant adenovirus; E1 region deficiency; gene therapy;
KW replication incompetent; ds.
XX
OS Mastadenovirus.
XX
PN WO200000628-A1.
XX
PD 06-JAN-2000.
XX
PF 24-JUN-1999; 99WO-US014333.
XX
PR 26-JUN-1998; 98US-00105515.
XX
PA (GENV-) GENVEC INC.
XX
PI Brough DE, Kovesdi I;
XX
DR WPI; 2000-147271/13.
XX
PT Novel replication-defective adenoviruses with a mutated major late
PT promoter used to study viral molecular genetics and as viral vectors for
PT genetic transfer.
XX
PS Disclosure; Page 18; 23pp; English.
XX
CC The invention relates to a recombinant adenovirus comprising a genome
CC with a deficiency in the E1 region and a mutation in the major late
CC promoter (MLP), so that the MLP is less active within a cell other than a
CC packaging cell. The recombinant adenoviruses are highly useful in
CC biological research. They can be used to study viral molecular genetics
CC and cytotoxicity, and to investigate the cell biology of viral growth and
CC infection. They can also be used to investigate molecular and cellular
CC biology of gene expression and regulation in novel genetic backgrounds,
CC e.g., interaction of gene products, ability of transcription factors to
CC transregulate gene expression via promoter, or enhancer elements
CC engineered into the adenovirus. The adenoviruses are also useful as gene
CC transfer vehicles, e.g., to introduce transgenes into tissues or cells,
CC and may thus be used as gene therapy vectors. The recombinant
CC adenoviruses can be grown without the presence of DNA complementary to
CC the wild type adenoviral MLP, substantially reducing the probability for
CC generating replication competent adenovirus (RCA). In addition, because
CC the viruses have a MLP which greatly attenuates L1-L5 gene expression in
CC nonpermissive host cells, they are less able than first generation
CC vectors to express late viral gene products in a host cell. Sequences
CC AAZ59957-Z59960 represent promoter elements of the MLP of adenovirus
CC serotype 5 (Ad5). The present sequence represents the upstream promoter
CC element (UPE), which is located 63 bp upstream of the transcriptional
CC start site
XX
SQ Sequence 12 BP; 2 A; 5 C; 4 G; 1 T; 0 U; 0 Other;

Query Match 42.0%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 37;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 GGTCACATGG 16
||||||.|||
Db 12 GGTCACGTGG 3

RESULT 58
AAA30866
ID AAA30866 standard; DNA; 12 BP.
XX
AC AAA30866;
XX
DT 19-SEP-2000 (first entry)
XX
DE Fragment of a plasmid for expressing a ubiquitin monomer.
XX
KW Ubiquitin monomer; protein production; plant cell; ubiquitin promoter;
KW plasmid fragment; ss.
XX
OS Unidentified.
XX
PN WO200036129-A1.
XX
PD 22-JUN-2000.
XX
PF 11-DEC-1998; 98WO-SG000103.
XX
PR 11-DEC-1998; 98WO-SG000103.
XX
PA (MOLE-) INST MOLECULAR AGROBIOLOGY.
XX
PI Fang R, Wu J, Chen X;
XX
DR WPI; 2000-431604/37.
XX
PT Production of desired protein in plants or plant cells by linking a
PT ubiquitin monomer coding sequence upstream of the gene encoding the
PT desired protein.
XX
PS Example 2; Page 20; 42pp; English.
XX
CC This sequence represents a fragment of a plasmid expressing a fusion
CC construct encoding a fusion protein having a ubiquitin monomer linked to
CC a protein of interest. The invention relates to a method for enhancing
CC production of a desired protein in a plant or plant cell by inserting a
CC nucleic acid (NA) encoding a ubiquitin monomer upstream of a NA encoding
CC the desired protein, where the fusion construct encodes a fusion protein
CC and expression is not controlled by the ubiquitin promoter. The invention
CC also relates to a NA acid vector a NA vector able to transform a plant
CC cell, that comprises NA encoding a fusion protein having a ubiquitin

```
CC   monomer linked to a protein of interest and further, where expression of
CC   the fusion construct is not under control of a ubiquitin promoter. The
CC   construct allows enhanced production of the desired protein in plants or
CC   plant cells
XX
SQ   Sequence 12 BP; 3 A; 3 C; 4 G; 2 T; 0 U; 0 Other;

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 12;
  Best Local Similarity   90.0%;  Pred. No. 37;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          8 GTCACATGGA 17
              ||| ||||||
Db          2 GTCGCATGGA 11


RESULT 59
ABI48155/c
ID   ABI48155 standard; DNA; 12 BP.
XX
AC   ABI48155;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide primer SEQ ID NO 348128 for detecting SNP TSC0045459.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 348128; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 12 BP; 4 A; 4 C; 0 G; 4 T; 0 U; 0 Other;

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 12;
  Best Local Similarity   90.0%;  Pred. No. 37;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         11 ACATGGATGA 20
              | ||||||||
Db         12 AGATGGATGA 3


RESULT 60
ABI35107
ID   ABI35107 standard; DNA; 12 BP.
XX
AC   ABI35107;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide primer SEQ ID NO 335080 for detecting SNP TSC0038590.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 335080; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 12 BP; 6 A; 0 C; 3 G; 3 T; 0 U; 0 Other;

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 12;
  Best Local Similarity   90.0%;  Pred. No. 37;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         11 ACATGGATGA 20
              | ||||||||
Db          2 AAATGGATGA 11


RESULT 61
ABI72389
ID   ABI72389 standard; DNA; 12 BP.
XX
AC   ABI72389;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide primer SEQ ID NO 372362 for detecting SNP TSC0059339.
XX
```

KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 372362; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 5 A; 0 C; 3 G; 4 T; 0 U; 0 Other;

Query Match 42.0%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 37;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 11 ACATGGATGA 20
|| ||||||||
Db 2 ATATGGATGA 11

RESULT 62
ABH84083/c
ID ABH84083 standard; DNA; 12 BP.
XX
AC ABH84083;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 284076 for detecting SNP TSC0011646.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 284076; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 4 A; 3 C; 0 G; 5 T; 0 U; 0 Other;

Query Match 42.0%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 37;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 11 ACATGGATGA 20
|| ||||||||
Db 11 ATATGGATGA 2

RESULT 63
ABI04761
ID ABI04761 standard; DNA; 12 BP.
XX
AC ABI04761;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 304734 for detecting SNP TSC0021079.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 304734; 29pp + Sequence Listing; German.
XX

```
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 12 BP; 4 A; 1 C; 5 G; 2 T; 0 U; 0 Other;

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 12;
  Best Local Similarity   90.0%;  Pred. No. 37;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         11 ACATGGATGA 20
              || |||||||
Db          2 ACGTGGATGA 11


RESULT 64
ABH67680
ID   ABH67680 standard; DNA; 12 BP.
XX
AC   ABH67680;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide primer SEQ ID NO 267657 for detecting SNP TSC0000420.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 267657; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 12 BP; 5 A; 0 C; 3 G; 4 T; 0 U; 0 Other;

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 12;
  Best Local Similarity   90.0%;  Pred. No. 37;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         11 ACATGGATGA 20
              | |||||||
Db          1 ATATGGATGA 10


RESULT 65
ABI08303/c
ID   ABI08303 standard; DNA; 12 BP.
XX
AC   ABI08303;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide primer SEQ ID NO 308276 for detecting SNP TSC0022938.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 308276; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 12 BP; 2 A; 5 C; 1 G; 4 T; 0 U; 0 Other;

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 12;
  Best Local Similarity   90.0%;  Pred. No. 37;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         11 ACATGGATGA 20
              || |||||||
Db         12 ACGTGGATGA 3


RESULT 66
ABI29750/c
```

ID ABI29750 standard; DNA; 12 BP.
XX
AC ABI29750;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 329723 for detecting SNP TSC0035111.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 329723; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 2 A; 3 C; 0 G; 7 T; 0 U; 0 Other;

Query Match 42.0%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 37;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 11 ACATGGATGA 20
|| ||||||||
Db 11 AAATGGATGA 2

RESULT 67
AAH49257
ID AAH49257 standard; DNA; 12 BP.
XX
AC AAH49257;
XX
DT 26-NOV-2001 (first entry)
XX
DE PNA-forming oligonucleotide #20.
XX
KW Polyamide-oligonucleotide derivative; anticancer; antiproliferative;
KW antiviral; hepatotropic; vasotropic; antisense inhibition; ribozyme;
KW integrin; cell-cell adhesion; cancer; restenosis; stability; PNA;
KW peptide nucleic acid; ss.
XX
OS Synthetic.
XX
PN EP1113021-A2.
XX
PD 04-JUL-2001.
XX
PF 08-MAR-1995; 2001EP-00104012.
XX
PR 14-MAR-1994; 94DE-04408528.
PR 08-MAR-1995; 95EP-00103332.
XX
PA (AVET) AVENTIS PHARMA DEUT GMBH.
XX
PI Uhlmann E, Breipohl G;
XX
DR WPI; 2001-591267/67.
XX
PT New DNA-peptide nucleic acid chimeras, useful e.g. as antisense agents
PT for treating e.g. cancer, also as diagnostic probes and primers.
XX
PS Example 43; Page 46; 54pp; German.
XX
CC This invention describes novel polyamide-oligonucleotide derivatives (I)
CC and their physiologically acceptable salts of formula F((DNA)-Li)_q(PNA-
CC Li)_r(DNA-Li)_s(PNA)_t)_xF' where q, r, s, t = 0 or 1, with the sum of
CC two or more adjacent letters at least 2; x = 1-20; DNA = nucleic acid
CC (such as DNA or RNA or their known derivatives); Li = covalent linkage
CC between DNA and PNA, i.e. a bond or a residue containing at least one
CC atom of carbon, nitrogen, oxygen or sulfur; PNA = polyamide structure
CC containing at least one nucleobase different from thymine; and F, F' =
CC end groups and/or are connected through a covalent bond. The products of
CC the invention have anticancer, antiproliferative, antiviral, hepatotropic
CC and vasotropic activity and can be used for the inhibition of gene
CC expression by antisense, ribozyme, sense, or triple-helix methods, or by
CC binding to proteins (aptamers). (I) are used for treating diseases caused
CC by viruses (human immune deficiency, herpes simplex, influenza, vesicular
CC stomatitis, hepatitis B or papilloma), or mediated by integrins or cell-
CC cell adhesion reactions, for treating cancer, or for inhibiting
CC restenosis, particularly as antisense reagents. They are also useful in
CC heterogeneous or homogeneous assays, as primers or probes, particularly
CC where the target is amplified before being detected by hybridization, for
CC diagnosis of genetic, malignant or pathogen-related diseases. (I) retain
CC the increased affinity for complementary strands and better stability in
CC serum, associated with conventional peptide nucleic acids (PNA), but lack
CC the disadvantages, i.e. have improved cellular uptake, do not aggregate
CC in aqueous solution, and have reduced affinity for purification
CC materials, reduced cytotoxicity, better sequence specificity. They are
CC more active than either DNA or PNA oligomers. When used as probes, (I)
CC show different responses to base-pair mismatches in the DNA and PNA
CC segments, allowing better discrimination between pathogenic and non-
CC pathogenic conditions such as the transition from proto-oncogene to
CC oncogene, also, when used as primers, with the PNA segment at the 5'-end,
CC they produce amplicons resistant to 5'-exonuclease, allowing this enzyme
CC to be used to eliminate RNA or DNA primers. The DNA component allows
CC additional reactions not possible with PNA alone, e.g. 3'-tailing and (I)
CC may be incorporated into a gene. AAH49208-AAH49264 represent
CC oligonucleotides used to illustrate the method of the invention
XX
SQ Sequence 12 BP; 3 A; 3 C; 3 G; 3 T; 0 U; 0 Other;

Query Match 42.0%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 37;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCTCATGGTC 10
| ||||||||
Db 2 CATCATGGTC 11

RESULT 68
AAH49256
ID AAH49256 standard; DNA; 12 BP.
XX

AC AAH49256;
XX
DT 26-NOV-2001 (first entry)
XX
DE PNA-forming oligonucleotide #19.
XX
KW Polyamide-oligonucleotide derivative; anticancer; antiproliferative;
KW antiviral; hepatotropic; vasotropic; antisense inhibition; ribozyme;
KW integrin; cell-cell adhesion; cancer; restenosis; stability; PNA;
KW peptide nucleic acid; ss.
XX
OS Synthetic.
XX
PN EP1113021-A2.
XX
PD 04-JUL-2001.
XX
PF 08-MAR-1995; 2001EP-00104012.
XX
PR 14-MAR-1994; 94DE-04408528.
PR 08-MAR-1995; 95EP-00103332.
XX
PA (AVET) AVENTIS PHARMA DEUT GMBH.
XX
PI Uhlmann E, Breipohl G;
XX
DR WPI; 2001-591267/67.
XX
PT New DNA-peptide nucleic acid chimeras, useful e.g. as antisense agents
PT for treating e.g. cancer, also as diagnostic probes and primers.
XX
PS Example 43; Page 46; 54pp; German.
XX
CC This invention describes novel polyamide-oligonucleotide derivatives (I)
CC and their physiologically acceptable salts of formula F((DNA)-Li)_q(PNA-
CC Li)_r(DNA-Li)_s(PNA)_t)_xF' where q, r, s, t = 0 or 1, with the sum of
CC two or more adjacent letters at least 2; x = 1-20; DNA = nucleic acid
CC (such as DNA or RNA or their known derivatives); Li = covalent linkage
CC between DNA and PNA, i.e. a bond or a residue containing at least one
CC atom of carbon, nitrogen, oxygen or sulfur; PNA = polyamide structure
CC containing at least one nucleobase different from thymine; and F, F' =
CC end groups and/or are connected through a covalent bond. The products of
CC the invention have anticancer, antiproliferative, antiviral, hepatotropic
CC and vasotropic activity and can be used for the inhibition of gene
CC expression by antisense, ribozyme, sense, or triple-helix methods, or by
CC binding to proteins (aptamers). (I) are used for treating diseases caused
CC by viruses (human immune deficiency, herpes simplex, influenza, vesicular
CC stomatitis, hepatitis B or papilloma), or mediated by integrins or cell-
CC cell adhesion reactions, for treating cancer, or for inhibiting
CC restenosis, particularly as antisense reagents. They are also useful in
CC heterogeneous or homogeneous assays, as primers or probes, particularly
CC where the target is amplified before being detected by hybridization, for
CC diagnosis of genetic, malignant or pathogen-related diseases. (I) retain
CC the increased affinity for complementary strands and better stability in
CC serum, associated with conventional peptide nucleic acids (PNA), but lack
CC the disadvantages, i.e. have improved cellular uptake, do not aggregate
CC in aqueous solution, and have reduced affinity for purification
CC materials, reduced cytotoxicity, better sequence specificity. They are
CC more active than either DNA or PNA oligomers. When used as probes, (I)
CC show different responses to base-pair mismatches in the DNA and PNA
CC segments, allowing better discrimination between pathogenic and non-
CC pathogenic conditions such as the transition from proto-oncogene to
CC oncogene, also, when used as primers, with the PNA segment at the 5'-end,
CC they produce amplicons resistant to 5'-exonuclease, allowing this enzyme
CC to be used to eliminate RNA or DNA primers. The DNA component allows
CC additional reactions not possible with PNA alone, e.g. 3'-tailing and (I)
CC may be incorporated into a gene. AAH49208-AAH49264 represent
CC oligonucleotides used to illustrate the method of the invention
XX
SQ Sequence 12 BP; 3 A; 3 C; 3 G; 3 T; 0 U; 0 Other;

Query Match 42.0%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 37;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCTCATGGTC 10
| ||||||||
Db 2 CATCATGGTC 11

RESULT 69
AAH49260
ID AAH49260 standard; DNA; 12 BP.
XX
AC AAH49260;
XX
DT 26-NOV-2001 (first entry)
XX
DE PNA-forming oligonucleotide #23.
XX
KW Polyamide-oligonucleotide derivative; anticancer; antiproliferative;
KW antiviral; hepatotropic; vasotropic; antisense inhibition; ribozyme;
KW integrin; cell-cell adhesion; cancer; restenosis; stability; PNA;
KW peptide nucleic acid; ss.
XX
OS Synthetic.
XX
PN EP1113021-A2.
XX
PD 04-JUL-2001.
XX
PF 08-MAR-1995; 2001EP-00104012.
XX
PR 14-MAR-1994; 94DE-04408528.
PR 08-MAR-1995; 95EP-00103332.
XX
PA (AVET) AVENTIS PHARMA DEUT GMBH.
XX
PI Uhlmann E, Breipohl G;
XX
DR WPI; 2001-591267/67.
XX
PT New DNA-peptide nucleic acid chimeras, useful e.g. as antisense agents
PT for treating e.g. cancer, also as diagnostic probes and primers.
XX
PS Example 43; Page 46; 54pp; German.
XX
CC This invention describes novel polyamide-oligonucleotide derivatives (I)
CC and their physiologically acceptable salts of formula F((DNA)-Li)_q(PNA-
CC Li)_r(DNA-Li)_s(PNA)_t)_xF' where q, r, s, t = 0 or 1, with the sum of
CC two or more adjacent letters at least 2; x = 1-20; DNA = nucleic acid
CC (such as DNA or RNA or their known derivatives); Li = covalent linkage
CC between DNA and PNA, i.e. a bond or a residue containing at least one
CC atom of carbon, nitrogen, oxygen or sulfur; PNA = polyamide structure
CC containing at least one nucleobase different from thymine; and F, F' =
CC end groups and/or are connected through a covalent bond. The products of
CC the invention have anticancer, antiproliferative, antiviral, hepatotropic
CC and vasotropic activity and can be used for the inhibition of gene
CC expression by antisense, ribozyme, sense, or triple-helix methods, or by
CC binding to proteins (aptamers). (I) are used for treating diseases caused
CC by viruses (human immune deficiency, herpes simplex, influenza, vesicular
CC stomatitis, hepatitis B or papilloma), or mediated by integrins or cell-
CC cell adhesion reactions, for treating cancer, or for inhibiting
CC restenosis, particularly as antisense reagents. They are also useful in
CC heterogeneous or homogeneous assays, as primers or probes, particularly
CC where the target is amplified before being detected by hybridization, for
CC diagnosis of genetic, malignant or pathogen-related diseases. (I) retain
CC the increased affinity for complementary strands and better stability in
CC serum, associated with conventional peptide nucleic acids (PNA), but lack
CC the disadvantages, i.e. have improved cellular uptake, do not aggregate
CC in aqueous solution, and have reduced affinity for purification
CC materials, reduced cytotoxicity, better sequence specificity. They are
CC more active than either DNA or PNA oligomers. When used as probes, (I)
CC show different responses to base-pair mismatches in the DNA and PNA
CC segments, allowing better discrimination between pathogenic and non-
CC pathogenic conditions such as the transition from proto-oncogene to

CC oncogene, also, when used as primers, with the PNA segment at the 5'-end,
CC they produce amplicons resistant to 5'-exonuclease, allowing this enzyme
CC to be used to eliminate RNA or DNA primers. The DNA component allows
CC additional reactions not possible with PNA alone, e.g. 3'-tailing and (I)
CC may be incorporated into a gene. AAH49208-AAH49264 represent
CC oligonucleotides used to illustrate the method of the invention
XX
SQ Sequence 12 BP; 3 A; 3 C; 3 G; 3 T; 0 U; 0 Other;

Query Match 42.0%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 37;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCTCATGGTC 10
|| ||||||||
Db 2 CATCATGGTC 11

RESULT 70
AAH49261
ID AAH49261 standard; DNA; 12 BP.
XX
AC AAH49261;
XX
DT 26-NOV-2001 (first entry)
XX
DE PNA-forming oligonucleotide #24.
XX
KW Polyamide-oligonucleotide derivative; anticancer; antiproliferative;
KW antiviral; hepatotropic; vasotropic; antisense inhibition; ribozyme;
KW integrin; cell-cell adhesion; cancer; restenosis; stability; PNA;
KW peptide nucleic acid; ss.
XX
OS Synthetic.
XX
PN EP1113021-A2.
XX
PD 04-JUL-2001.
XX
PF 08-MAR-1995; 2001EP-00104012.
XX
PR 14-MAR-1994; 94DE-04408528.
PR 08-MAR-1995; 95EP-00103332.
XX
PA (AVET) AVENTIS PHARMA DEUT GMBH.
XX
PI Uhlmann E, Breipohl G;
XX
DR WPI; 2001-591267/67.
XX
PT New DNA-peptide nucleic acid chimeras, useful e.g. as antisense agents
PT for treating e.g. cancer, also as diagnostic probes and primers.
XX
PS Example 43; Page 46; 54pp; German.
XX
CC This invention describes novel polyamide-oligonucleotide derivatives (I)
CC and their physiologically acceptable salts of formula F((DNA)-Li)_q(PNA-
CC Li)_r(DNA-Li)_s(PNA)_t)_xF' where q, r, s, t = 0 or 1, with the sum of
CC two or more adjacent letters at least 2; x = 1-20; DNA = nucleic acid
CC (such as DNA or RNA or their known derivatives); Li = covalent linkage
CC between DNA and PNA, i.e. a bond or a residue containing at least one
CC atom of carbon, nitrogen, oxygen or sulfur; PNA = polyamide structure
CC containing at least one nucleobase different from thymine; and F, F' =
CC end groups and/or are connected through a covalent bond. The products of
CC the invention have anticancer, antiproliferative, antiviral, hepatotropic
CC and vasotropic activity and can be used for the inhibition of gene
CC expression by antisense, ribozyme, sense, or triple-helix methods, or by
CC binding to proteins (aptamers). (I) are used for treating diseases caused
CC by viruses (human immune deficiency, herpes simplex, influenza, vesicular
CC stomatitis, hepatitis B or papilloma), or mediated by integrins or cell-
CC cell adhesion reactions, for treating cancer, or for inhibiting
CC restenosis, particularly as antisense reagents. They are also useful in
CC heterogeneous or homogeneous assays, as primers or probes, particularly
CC where the target is amplified before being detected by hybridization, for
CC diagnosis of genetic, malignant or pathogen-related diseases. (I) retain
CC the increased affinity for complementary strands and better stability in
CC serum, associated with conventional peptide nucleic acids (PNA), but lack
CC the disadvantages, i.e. have improved cellular uptake, do not aggregate
CC in aqueous solution, and have reduced affinity for purification
CC materials, reduced cytotoxicity, better sequence specificity. They are
CC more active than either DNA or PNA oligomers. When used as probes, (I)
CC show different responses to base-pair mismatches in the DNA and PNA
CC segments, allowing better discrimination between pathogenic and non-
CC pathogenic conditions such as the transition from proto-oncogene to
CC oncogene, also, when used as primers, with the PNA segment at the 5'-end,
CC they produce amplicons resistant to 5'-exonuclease, allowing this enzyme
CC to be used to eliminate RNA or DNA primers. The DNA component allows
CC additional reactions not possible with PNA alone, e.g. 3'-tailing and (I)
CC may be incorporated into a gene. AAH49208-AAH49264 represent
CC oligonucleotides used to illustrate the method of the invention
XX
SQ Sequence 12 BP; 3 A; 3 C; 3 G; 3 T; 0 U; 0 Other;

Query Match 42.0%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 37;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCTCATGGTC 10
|| ||||||||
Db 2 CATCATGGTC 11

RESULT 71
AAH49259
ID AAH49259 standard; DNA; 12 BP.
XX
AC AAH49259;
XX
DT 26-NOV-2001 (first entry)
XX
DE PNA-forming oligonucleotide #22.
XX
KW Polyamide-oligonucleotide derivative; anticancer; antiproliferative;
KW antiviral; hepatotropic; vasotropic; antisense inhibition; ribozyme;
KW integrin; cell-cell adhesion; cancer; restenosis; stability; PNA;
KW peptide nucleic acid; ss.
XX
OS Synthetic.
XX
PN EP1113021-A2.
XX
PD 04-JUL-2001.
XX
PF 08-MAR-1995; 2001EP-00104012.
XX
PR 14-MAR-1994; 94DE-04408528.
PR 08-MAR-1995; 95EP-00103332.
XX
PA (AVET) AVENTIS PHARMA DEUT GMBH.
XX
PI Uhlmann E, Breipohl G;
XX
DR WPI; 2001-591267/67.
XX
PT New DNA-peptide nucleic acid chimeras, useful e.g. as antisense agents
PT for treating e.g. cancer, also as diagnostic probes and primers.
XX
PS Example 43; Page 46; 54pp; German.
XX
CC This invention describes novel polyamide-oligonucleotide derivatives (I)
CC and their physiologically acceptable salts of formula F((DNA)-Li)_q(PNA-
CC Li)_r(DNA-Li)_s(PNA)_t)_xF' where q, r, s, t = 0 or 1, with the sum of
CC two or more adjacent letters at least 2; x = 1-20; DNA = nucleic acid
CC (such as DNA or RNA or their known derivatives); Li = covalent linkage
CC between DNA and PNA, i.e. a bond or a residue containing at least one
CC atom of carbon, nitrogen, oxygen or sulfur; PNA = polyamide structure

```
CC   containing at least one nucleobase different from thymine; and F, F' =
CC   end groups and/or are connected through a covalent bond. The products of
CC   the invention have anticancer, antiproliferative, antiviral, hepatotropic
CC   and vasotropic activity and can be used for the inhibition of gene
CC   expression by antisense, ribozyme, sense, or triple-helix methods, or by
CC   binding to proteins (aptamers). (I) are used for treating diseases caused
CC   by viruses (human immune deficiency, herpes simplex, influenza, vesicular
CC   stomatitis, hepatitis B or papilloma), or mediated by integrins or cell-
CC   cell adhesion reactions, for treating cancer, or for inhibiting
CC   restenosis, particularly as antisense reagents. They are also useful in
CC   heterogeneous or homogeneous assays, as primers or probes, particularly
CC   where the target is amplified before being detected by hybridization, for
CC   diagnosis of genetic, malignant or pathogen-related diseases. (I) retain
CC   the increased affinity for complementary strands and better stability in
CC   serum, associated with conventional peptide nucleic acids (PNA), but lack
CC   the disadvantages, i.e. have improved cellular uptake, do not aggregate
CC   in aqueous solution, and have reduced affinity for purification
CC   materials, reduced cytotoxicity, better sequence specificity. They are
CC   more active than either DNA or PNA oligomers. When used as probes, (I)
CC   show different responses to base-pair mismatches in the DNA and PNA
CC   segments, allowing better discrimination between pathogenic and non-
CC   pathogenic conditions such as the transition from proto-oncogene to
CC   oncogene, also, when used as primers, with the PNA segment at the 5'-end,
CC   they produce amplicons resistant to 5'-exonuclease, allowing this enzyme
CC   to be used to eliminate RNA or DNA primers. The DNA component allows
CC   additional reactions not possible with PNA alone, e.g. 3'-tailing and (I)
CC   may be incorporated into a gene. AAH49208-AAH49264 represent
CC   oligonucleotides used to illustrate the method of the invention
XX
SQ   Sequence 12 BP; 3 A; 3 C; 3 G; 3 T; 0 U; 0 Other;

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 12;
  Best Local Similarity   90.0%;  Pred. No. 37;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 CCTCATGGTC 10
              | ||||||||
Db          2 CATCATGGTC 11


RESULT 72
AAH49258
ID   AAH49258 standard; DNA; 12 BP.
XX
AC   AAH49258;
XX
DT   26-NOV-2001  (first entry)
XX
DE   PNA-forming oligonucleotide #21.
XX
KW   Polyamide-oligonucleotide derivative; anticancer; antiproliferative;
KW   antiviral; hepatotropic; vasotropic; antisense inhibition; ribozyme;
KW   integrin; cell-cell adhesion; cancer; restenosis; stability; PNA;
KW   peptide nucleic acid; ss.
XX
OS   Synthetic.
XX
PN   EP1113021-A2.
XX
PD   04-JUL-2001.
XX
PF   08-MAR-1995; 2001EP-00104012.
XX
PR   14-MAR-1994;   94DE-04408528.
PR   08-MAR-1995;   95EP-00103332.
XX
PA   (AVET ) AVENTIS PHARMA DEUT GMBH.
XX
PI   Uhlmann E,  Breipohl G;
XX
DR   WPI; 2001-591267/67.
XX
PT   New DNA-peptide nucleic acid chimeras, useful e.g. as antisense agents
PT   for treating e.g. cancer, also as diagnostic probes and primers.
XX
PS   Example 43; Page 46; 54pp; German.
XX
CC   This invention describes novel polyamide-oligonucleotide derivatives (I)
CC   and their physiologically acceptable salts of formula F((DNA)-Li)_q(PNA-
CC   Li)_r(DNA-Li)_s(PNA)_t)_xF' where q, r, s, t = 0 or 1, with the sum of
CC   two or more adjacent letters at least 2; x = 1-20; DNA = nucleic acid
CC   (such as DNA or RNA or their known derivatives); Li = covalent linkage
CC   between DNA and PNA, i.e. a bond or a residue containing at least one
CC   atom of carbon, nitrogen, oxygen or sulfur; PNA = polyamide structure
CC   containing at least one nucleobase different from thymine; and F, F' =
CC   end groups and/or are connected through a covalent bond. The products of
CC   the invention have anticancer, antiproliferative, antiviral, hepatotropic
CC   and vasotropic activity and can be used for the inhibition of gene
CC   expression by antisense, ribozyme, sense, or triple-helix methods, or by
CC   binding to proteins (aptamers). (I) are used for treating diseases caused
CC   by viruses (human immune deficiency, herpes simplex, influenza, vesicular
CC   stomatitis, hepatitis B or papilloma), or mediated by integrins or cell-
CC   cell adhesion reactions, for treating cancer, or for inhibiting
CC   restenosis, particularly as antisense reagents. They are also useful in
CC   heterogeneous or homogeneous assays, as primers or probes, particularly
CC   where the target is amplified before being detected by hybridization, for
CC   diagnosis of genetic, malignant or pathogen-related diseases. (I) retain
CC   the increased affinity for complementary strands and better stability in
CC   serum, associated with conventional peptide nucleic acids (PNA), but lack
CC   the disadvantages, i.e. have improved cellular uptake, do not aggregate
CC   in aqueous solution, and have reduced affinity for purification
CC   materials, reduced cytotoxicity, better sequence specificity. They are
CC   more active than either DNA or PNA oligomers. When used as probes, (I)
CC   show different responses to base-pair mismatches in the DNA and PNA
CC   segments, allowing better discrimination between pathogenic and non-
CC   pathogenic conditions such as the transition from proto-oncogene to
CC   oncogene, also, when used as primers, with the PNA segment at the 5'-end,
CC   they produce amplicons resistant to 5'-exonuclease, allowing this enzyme
CC   to be used to eliminate RNA or DNA primers. The DNA component allows
CC   additional reactions not possible with PNA alone, e.g. 3'-tailing and (I)
CC   may be incorporated into a gene. AAH49208-AAH49264 represent
CC   oligonucleotides used to illustrate the method of the invention
XX
SQ   Sequence 12 BP; 3 A; 3 C; 3 G; 3 T; 0 U; 0 Other;

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 12;
  Best Local Similarity   90.0%;  Pred. No. 37;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 CCTCATGGTC 10
              | ||||||||
Db          2 CATCATGGTC 11


RESULT 73
ABA82718/c
ID   ABA82718 standard; DNA; 12 BP.
XX
AC   ABA82718;
XX
DT   07-FEB-2002  (first entry)
XX
DE   Human protective DNA sequence CNI-00735 fragment #4.
XX
KW   Human; protective sequence; cell death; cancer; autoimmune disease;
KW   neurological disorder; stroke; cytostatic; neuroprotective; gene therapy;
KW   ds.
XX
OS   Homo sapiens.
XX
PN   WO200176457-A2.
XX
PD   18-OCT-2001.
XX
PF   09-APR-2001; 2001WO-US011663.
XX
```

PR 11-APR-2000; 2000US-00547735.
XX
PA (COGE-) COGENT NEUROSCIENCE INC.
XX
PI Thomas MB, Portbury SD, Puranam K, Katz LC, Lo DC, Barney S;
XX
DR WPI; 2002-025874/03.
XX
PT New protective sequences and their products, useful for diagnosing and
PT treating diseases involving cell death, including neurological disorders
PT e.g. stroke and for identifying modulators of expression of the
PT protective sequences.
XX
PS Claim 2; Fig 5; 283pp; English.
XX
CC The present invention relates to protective sequence proteins (ABB44624-
CC ABB44830) and their coding sequences (ABA82701-ABA82937). The sequences,
CC when introduced into a cell either predisposed to undergo cell death or
CC in the process of undergoing cell death, prevent, delay or rescue the
CC cell from death, hence, these sequences are named "protective sequences".
CC The sequences are useful for treating and/or ameliorating cancer,
CC autoimmune diseases and neurological disorders e.g. stroke. Further
CC examples of diseases which may be treated by the present invention are
CC given in the specification
XX
SQ Sequence 12 BP; 4 A; 2 C; 3 G; 3 T; 0 U; 0 Other;

Query Match 42.0%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 37;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 CTCATGGTCA 11
|||||||||
Db 11 CACATGGTCA 2

RESULT 74
ABK72560
ID ABK72560 standard; DNA; 12 BP.
XX
AC ABK72560;
XX
DT 13-AUG-2002 (first entry)
XX
DE Human OPA1 gene, exon/intron junction #27.
XX
KW Human; ophthalmological; OPA1; autosomal dominant optic atrophy; ADOA;
KW gene; ds.
XX
OS Homo sapiens.
XX
PN WO200227022-A2.
XX
PD 04-APR-2002.
XX
PF 26-SEP-2001; 2001WO-GB004284.
XX
PR 26-SEP-2000; 2000GB-00023555.
XX
PA (UNLO) UNIV COLLEGE LONDON.
PA (UYEY-) UNIV EYE HOSPITAL.
XX
PI Bhattacharya S, Wissinger B, Alexander C, Votruba M;
XX
DR WPI; 2002-416484/44.
XX
PT Novel human normal or mutant OPA1 (the predominant locus for autosomal
PT dominant optic atrophy (ADOA)) polypeptides and the OPA1 gene, useful in
PT the diagnosis and treatment of autosomal dominant optic atrophy ADOA.
XX
PS Disclosure; Fig 12; 75pp; English.
XX
CC The invention relates to an isolated human normal or mutant OPA1 (the
CC predominant locus for autosomal dominant optic atrophy (ADOA))
CC polypeptide (I), characterised by a molecular weight of about 112 kDa,
CC and substantially free of other human proteins. Also described is the DNA
CC (II) encoding (I). (I) and (II) are useful as a medicament, for the
CC treatment of a medical condition resulting from a defect in the OPA1
CC gene, which results in autosomal dominant optic atrophy. The nucleic acid
CC and antibodies to (I) are useful in a variety of hybridisation and
CC immunological assays to screen for, and to detect the presence of, either
CC a normal or a defective OPA1 gene or gene product. ABK72533-ABK72593
CC represent the human OPA1 gene and intron/exon splice junctions
XX
SQ Sequence 12 BP; 3 A; 1 C; 3 G; 5 T; 0 U; 0 Other;

Query Match 42.0%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 37;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 9 TCACATGGAT 18
||| ||||||
Db 3 TCAGATGGAT 12

RESULT 75
ABA01332/c
ID ABA01332 standard; RNA; 12 BP.
XX
AC ABA01332;
XX
DT 29-AUG-2003 (revised)
DT 03-JUL-2002 (first entry)
XX
DE HIV-1 rev oligonucleotide #5.
XX
KW Selenoprotein; HIV; Ebola virus; cancer; immune system disorder; ss.
XX
OS Human immunodeficiency virus 1.
XX
PN US6303295-B1.
XX
PD 16-OCT-2001.
XX
PF 12-JUL-1996; 96US-00679493.
XX
PR 14-JUL-1995; 95US-0001203P.
PR 01-SEP-1995; 95US-0003112P.
XX
PA (UYGE-) UNIV GEORGIA RES FOUND INC.
XX
PI Taylor EW, Nadimpalli RG, Ramanathan CS;
XX
DR WPI; 2002-024734/03.
XX
PT New selenoprotein for use in detecting certain viruses, e.g. human
PT immunodeficiency virus (HIV) or Ebola, cancer and immune system
PT disorders.
XX
PS Disclosure; Col 26; 140pp; English.
XX
CC The present invention relates to selenoproteins encoded in the genome of
CC a virus, where the coding sequence of the selenoprotein is genetically
CC engineered for expression in a nucleic acid construct. The invention also
CC discloses a method for identifying selenoprotein coding sequences, for
CC detecting certain viruses (e.g. HIV or Ebola), cancer and immune system
CC disorders. The present sequence was used to illustrate the invention.
CC (Updated on 29-AUG-2003 to standardise OS field)
XX
SQ Sequence 12 BP; 4 A; 3 C; 3 G; 0 T; 2 U; 0 Other;

Query Match 42.0%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 37;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 CTCATGGTCA 11

```
                ||||| |||||
Db          11 CTCAGGGTCA 2


RESULT 76
AAK98610
ID   AAK98610 standard; DNA; 12 BP.
XX
AC   AAK98610;
XX
DT   16-APR-2002  (first entry)
XX
DE   Modified peptide nucleic acid #1.
XX
KW   Peptide nucleic acid; PNA; polyamide backbone; phosphoryl radical;
KW   cytostatic; virucide; dermatological; antiasthmatic; cancer; antisense;
KW   viral infection; vitiligo; pigmentation disorder; asthma; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "modified by phosphate and N-(2-
FT                   hydroxyethyl)glycine"
FT   modified_base   12
FT                   /*tag=  b
FT                   /mod_base= OTHER
FT                   /note= "modified by hex"
XX
PN   WO200179249-A2.
XX
PD   25-OCT-2001.
XX
PF   07-APR-2001; 2001WO-EP004027.
XX
PR   18-APR-2000; 2000DE-01019136.
XX
PA   (AVET ) AVENTIS PHARMA DEUT GMBH.
XX
PI   Uhlmann E,  Breipohl G,  Will DW;
XX
DR   WPI; 2002-089643/12.
XX
PT   New peptide nucleic acid derivatives, useful e.g. for treating tumors and
PT   diagnosis, have N-terminal phosphoryl residue for improving e.g.
PT   solubility in water.
XX
PS   Example 3; Page 38; 96pp; German.
XX
CC   The present invention relates to peptide nucleic acid (PNA) derivatives.
CC   These can be used in the treatment of cancer, viral infections, vitiligo
CC   or other pigmentation disorders, and asthma. The present sequence is an
CC   oligonucleotide fragment of a PNA described in the exemplification of the
CC   invention
XX
SQ   Sequence 12 BP; 3 A; 3 C; 3 G; 3 T; 0 U; 0 Other;

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 12;
  Best Local Similarity   90.0%;  Pred. No. 37;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 CCTCATGGTC 10
              | ||||||||
Db          2 CATCATGGTC 11


RESULT 77
ABA97503
ID   ABA97503 standard; DNA; 12 BP.
XX
AC   ABA97503;
XX
DT   16-APR-2002  (first entry)
XX
DE   Peptide nucleic acid SEQ ID NO: 50.
XX
KW   Peptide nucleic acid; PNA; polyamide backbone; phosphoryl radical;
KW   cytostatic; virucide; dermatological; antiasthmatic; cancer; antisense;
KW   viral infection; vitiligo; pigmentation disorder; asthma; ss.
XX
OS   Synthetic.
XX
PN   WO200179249-A2.
XX
PD   25-OCT-2001.
XX
PF   07-APR-2001; 2001WO-EP004027.
XX
PR   18-APR-2000; 2000DE-01019136.
XX
PA   (AVET ) AVENTIS PHARMA DEUT GMBH.
XX
PI   Uhlmann E,  Breipohl G,  Will DW;
XX
DR   WPI; 2002-089643/12.
XX
PT   New peptide nucleic acid derivatives, useful e.g. for treating tumors and
PT   diagnosis, have N-terminal phosphoryl residue for improving e.g.
PT   solubility in water.
XX
PS   Disclosure; Page 91; 96pp; German.
XX
CC   The present invention relates to peptide nucleic acid (PNA) derivatives.
CC   These can be used in the treatment of cancer, viral infections, vitiligo
CC   or other pigmentation disorders, and asthma. The present sequence is an
CC   oligonucleotide fragment of a PNA described in the exemplification of the
CC   invention
XX
SQ   Sequence 12 BP; 3 A; 3 C; 3 G; 3 T; 0 U; 0 Other;

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 12;
  Best Local Similarity   90.0%;  Pred. No. 37;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 CCTCATGGTC 10
              | ||||||||
Db          2 CATCATGGTC 11


RESULT 78
ADM56294/c
ID   ADM56294 standard; DNA; 12 BP.
XX
AC   ADM56294;
XX
DT   03-JUN-2004  (first entry)
XX
DE   Mouse SLC26A6 anion transporter protein gene splice site #13.
XX
KW   SLC26A6; SLC26A1; SLC26A2; anion transporter protein; cancer;
KW   splice site; ds; mouse; murine.
XX
OS   Mus musculus.
XX
PN   WO2003072759-A2.
XX
PD   04-SEP-2003.
XX
PF   28-FEB-2003; 2003WO-US006469.
XX
PR   28-FEB-2002; 2002US-0360275P.
XX
PA   (UYVA-) UNIV VANDERBILT.
PA   (UYCA-) UNIV CASE WESTERN RESERVE.
```

PA (BGHM) BRIGHAM & WOMENS HOSPITAL.
XX
PI Mount DB, Romero MF;
XX
DR WPI; 2003-712726/67.
XX
PT New SLC26A6, SLC26A1 or SLC26A2 polypeptide, useful for preparing a
PT composition for treating e.g., cancer.
XX
PS Example 2; SEQ ID NO 26; 204pp; English.
XX
CC The invention comprises the amino acid and coding sequences of SLC26A6,
CC SLC26A1 and SLC26A2 anion transporter proteins. The DNA and protein
CC sequences of the invention are useful for treating cancer. The present
CC DNA sequence represents a splice site from the gene encoding the mouse
CC SLC26A6 anion transporter protein.
XX
SQ Sequence 12 BP; 3 A; 1 C; 3 G; 5 T; 0 U; 0 Other;

Query Match 42.0%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 37;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 9 TCACATGGAT 18
|||||| |||
Db 10 TCACATAGAT 1

RESULT 79
ADQ29965
ID ADQ29965 standard; DNA; 12 BP.
XX
AC ADQ29965;
XX
DT 09-SEP-2004 (first entry)
XX
DE Rat VR1 exon 1d transcription factor binding fragment #41.
XX
KW ds; VR1 receptor; vanilloid receptor type 1; modulator;
KW pain transmission; primary sensory neuron; transcription factor;
KW detection; MZF1; NFkappaB; NFAT; GATA1; sensitivity disorder; analgesia;
KW hypalgesia; hyperalgesia; neuralgia; myalgia; rat.
XX
OS Rattus sp.
XX
PN WO2004053120-A2.
XX
PD 24-JUN-2004.
XX
PF 01-DEC-2003; 2003WO-EP013522.
XX
PR 09-DEC-2002; 2002DE-01057421.
XX
PA (CHEF) GRUENENTHAL GMBH.
XX
PI Weihe E, Bieller A, Schaefer MKH;
XX
DR WPI; 2004-468868/44.
XX
PT New nucleic acid that modulates expression of the vanilloid receptor-1,
PT useful for control of pain or sensitivity disorders, comprises sequences
PT from control regions of the receptor gene.
XX
PS Disclosure; Page 46; 68pp; German.
XX
CC This invention describes a novel nucleic acid containing a specific
CC segment having at least one region that modulates expression of the VR1
CC (vanilloid receptor type 1) receptor, or a functional derivative, allele
CC or fragment of this region, or a sequence that hybridises to it under
CC standard conditions. The VR1 modulator is derived from one or more of
CC positions 221931-223344 of GenBank AL670399, 31673-36359 of AL663116, or
CC 44731-43231 or 36616-33151 of AF168787 and is involved in transmission of
CC pain, particularly in primary sensory neurons. The invention also
CC describes a vector that contains the VR1 modulator, host cells containing
CC this vector (other than human germ or embryonal stem cells) and a method
CC for modulating expression of the VR1 receptor by introducing the
CC modulator or the vector into a cell that contains the VR1 gene. The
CC products of the invention are used for detecting a transcription factor
CC from its binding to a regulatory sequence (or a double-stranded
CC oligonucleotide fragment of it), e.g. by Western blotting or enzyme-
CC linked immunosorbant assay, particularly for diagnosis of diseases
CC associated with overexpression or underexpression of the transcription
CC factor. The region that modulates VR1 receptor expression includes a
CC binding site for a transcription factor, e.g. MZF1, NFkappaB, NFAT or
CC GATA1. The nucleic acids of the invention, or vectors containing them,
CC are used for prevention or treatment of pain, also for treating
CC sensitivity disorders, e.g. analgesia, hypalgesia or hyperalgesia, also
CC neuralgia and myalgia, that are associated with activity of the VR1
CC receptor. This sequence represents a fragment of rat VR1 exon 1d DNA
CC which is capable of binding to a transcription factor.
XX
SQ Sequence 12 BP; 3 A; 2 C; 6 G; 1 T; 0 U; 0 Other;

Query Match 42.0%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 37;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 10 CACATGGATG 19
|||| |||||
Db 1 CACAGGGATG 10

RESULT 80
AEF80873/c
ID AEF80873 standard; DNA; 12 BP.
XX
AC AEF80873;
XX
DT 20-APR-2006 (first entry)
XX
DE MLTF/USF promoter target DNA fragment.
XX
KW Gene expression; gene regulation; platinum zinc complex; cancer; tumor;
KW neoplasm; promoter; target; ds.
XX
OS Unidentified.
XX
PN JP2006045131-A.
XX
PD 16-FEB-2006.
XX
PF 05-AUG-2004; 2004JP-00229182.
XX
PR 05-AUG-2004; 2004JP-00229182.
XX
PA (UYTK) UNIV TOKYO RIKA GH.
XX
PI Aoki S, Okaya R, Takeda T, Kimura E;
XX
DR WPI; 2006-150505/16.
XX
PT Novel platinum-zinc complex useful as agent for controlling expression of
PT promoter sequence or RNA of specific gene for treatment of cancer.
XX
PS Example 4; Page 10; 21pp; Japanese.
XX
CC The invention relates to a novel platinum-zinc complex (C1) used in the
CC regulation of gene expression. The complex of the invention is prepared
CC by reacting a 2,2'-bipyridyl derivative and a cyclen derivative protected
CC by t-butoxycarbonyl (Boc), adding the platinum compound to the obtained
CC complex. (C1) is useful as an agent for controlling the expression of a
CC specific gene. This involves contacting (C1) with the nucleic acid
CC sequence of the gene, where the nucleic acid sequence is a promoter
CC sequence which controls the expression of the gene, or an RNA encoding
CC the gene. The platinum complex in (C1) has increased anti-tumor activity
CC with respect to solid tumors such as testicular tumors, ovarian cancer,

CC head and neck cancer, esophageal cancer and small cell lung carcinoma.
CC (C1) controls the gene expression by the combination of zinc and platinum
CC complex in its structure. The current sequence represents a promoter
CC fragment that may act as a target for the complex of the invention.
XX
SQ Sequence 12 BP; 2 A; 5 C; 4 G; 1 T; 0 U; 0 Other;

Query Match 42.0%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 37;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 GGTCACATGG 16
||||||.|||
Db 12 GGTCACGTGG 3

Search completed: June 13, 2006, 15:46:02
Job time : 0.001 secs

OM nucleic - nucleic search, using sw model

Run on: June 13, 2006, 15:44:11 ; Search time 0.001 Seconds
(without alignments)
18.680 Million cell updates/sec

Title: US-10-719-370A-446
Perfect score: 20
Sequence: 1 cctcatggtcacatggatga 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 0.5

Searched: 36 seqs, 467 residues

Total number of hits satisfying chosen parameters: 72

Minimum DB seq length: 12
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 36 summaries

Database : us-10-719-370a-446.sl.rge4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
c	1	17	85.0	20	1	CS097426	ACCESSION:CS097426
	2	14.8	74.0	19	1	AR199401	ACCESSION:AR199401
c	3	12.8	64.0	17	1	AX732438	ACCESSION:AX732438
c	4	12.2	61.0	17	1	CQ622872	ACCESSION:CQ622872
c	5	12.2	61.0	17	1	AR463935	ACCESSION:AR463935
	6	10.8	54.0	15	1	AR180445	ACCESSION:AR180445
	7	9.4	47.0	12	1	A71522	ACCESSION:A71522
	8	9.4	47.0	12	1	S74610	ACCESSION:S74610
	9	9.4	47.0	13	1	AR759769	ACCESSION:AR759769
c	10	9.4	47.0	13	1	AR759770	ACCESSION:AR759770
c	11	9	45.0	12	1	AR058623	ACCESSION:AR058623
	12	8.8	44.0	12	1	I04322	ACCESSION:I04322
c	13	8.4	42.0	12	1	AR024074	ACCESSION:AR024074
c	14	8.4	42.0	12	1	AR075457	ACCESSION:AR075457
c	15	8.4	42.0	12	1	AR108947	ACCESSION:AR108947
c	16	8.4	42.0	12	1	AR153908	ACCESSION:AR153908
c	17	8.4	42.0	12	1	AR172244	ACCESSION:AR172244
c	18	8.4	42.0	12	1	AR178525	ACCESSION:AR178525
c	19	8.4	42.0	12	1	BD001178	ACCESSION:BD001178
c	20	8.4	42.0	12	1	BD001607	ACCESSION:BD001607
c	21	8.4	42.0	12	1	BD064941	ACCESSION:BD064941
c	22	8.4	42.0	12	1	BD240723	ACCESSION:BD240723
	23	8.4	42.0	12	1	BD261806	ACCESSION:BD261806
	24	8.4	42.0	12	1	CQ828540	ACCESSION:CQ828540
c	25	8.4	42.0	12	1	I17542	ACCESSION:I17542
c	26	8.4	42.0	12	1	AR224293	ACCESSION:AR224293
c	27	8.4	42.0	12	1	AR234464	ACCESSION:AR234464
c	28	8.4	42.0	12	1	AR275829	ACCESSION:AR275829
c	29	8.4	42.0	12	1	I58612	ACCESSION:I58612
c	30	8.4	42.0	12	1	I72395	ACCESSION:I72395
	31	8.4	42.0	12	1	AR577337	ACCESSION:AR577337
	32	8.4	42.0	12	1	AR699868	ACCESSION:AR699868
	33	8.4	42.0	12	1	AR699877	ACCESSION:AR699877
c	34	8.4	42.0	12	1	AR699878	ACCESSION:AR699878
	35	8.4	42.0	12	1	AX283286	ACCESSION:AX283286
c	36	8.4	42.0	12	1	AX711060	ACCESSION:AX711060

ALIGNMENTS

RESULT 1
CS097426/c
LOCUS CS097426 20 bp DNA linear PAT 03-JUN-2005
DEFINITION Sequence 69 from Patent WO2005045070.
ACCESSION CS097426
VERSION CS097426.1 GI:66953875
KEYWORDS .
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Lacroix,B., Krause,A., Puisieux,A. and Bachelot,T.
TITLE Method for prognosticating a breast cancer
JOURNAL Patent: WO 2005045070-A 69 19-MAY-2005;
BIOMERIEUX (FR); Centre Leon Berard (FR)
FEATURES Location/Qualifiers
source 1. .20
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 85.0%; Score 17; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.55;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTCATGGTCACATGGA 17
||||||||||||||||
Db 17 CCTCATGGTCACATGGA 1

RESULT 2
AR199401
LOCUS AR199401 19 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 22 from patent US 6355434.
ACCESSION AR199401
VERSION AR199401.1 GI:20249475
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 19)
AUTHORS Drazen,J.M., In,K.-H., Asano,K., Beier,D. and Grobholz,J.
TITLE 5-Lipoxygenase gene polymorphisms and their use in classifying patients
JOURNAL Patent: US 6355434-A 22 12-MAR-2002;
FEATURES Location/Qualifiers
source 1. .19
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 74.0%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred. No. 1.5;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CTCATGGTCACATGGATG 19
|||||| ||| |||||||
Db 2 CTCATGCTCAGATGGATG 19

RESULT 3
AX732438/c
LOCUS AX732438 17 bp DNA linear PAT 08-MAY-2003
DEFINITION Sequence 4072 from Patent WO03025175.

```
ACCESSION   AX732438
VERSION     AX732438.1  GI:30511781
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Telerman,A., Amson,R. and Tuijnder,M.
  TITLE     Sequences involved in phenomena of tumour suppression, tumour
            reversion, apoptosis and/or virus resistance and their use as
            medicines
  JOURNAL   Patent: WO 03025175-A 4072 27-MAR-2003;
            Molecular Engines Laboratories (FR)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match            64.0%;  Score 12.8;  DB 1;  Length 17;
  Best Local Similarity  87.5%;  Pred. No. 3.3;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          3 TCATGGTCACATGGAT 18
              ||| ||||| ||||||
Db         17 TCAAGGTCAAATGGAT 2


RESULT 4
CQ622872/c
LOCUS       CQ622872                  17 bp    DNA     linear   PAT 02-FEB-2004
DEFINITION  Sequence 7612 from Patent WO0192524.
ACCESSION   CQ622872
VERSION     CQ622872.1  GI:41673090
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and
            Shannon,M.E.
  TITLE     Myosin-like gene expressed in human heart and muscle
  JOURNAL   Patent: WO 0192524-A 7612 06-DEC-2001;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match            61.0%;  Score 12.2;  DB 1;  Length 17;
  Best Local Similarity  82.4%;  Pred. No. 4.5;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 CCTCATGGTCACATGGA 17
              ||||| ||||||| | |
Db         17 CCTCAAGGTCACAGGTA 1


RESULT 5
AR463935/c
LOCUS       AR463935                  17 bp    DNA     linear   PAT 20-FEB-2004
DEFINITION  Sequence 7612 from patent US 6686188.
ACCESSION   AR463935
VERSION     AR463935.1  GI:42698992
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and
            Shannon,M.E.
  TITLE     Polynucleotide encoding a human myosin-like polypeptide expressed
            predominantly in heart and muscle
  JOURNAL   Patent: US 6686188-A 7612 03-FEB-2004;
            Amersham PLC; Buckinghamshire;
            GBX;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match            61.0%;  Score 12.2;  DB 1;  Length 17;
  Best Local Similarity  82.4%;  Pred. No. 4.5;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 CCTCATGGTCACATGGA 17
              ||||| ||||||| | |
Db         17 CCTCAAGGTCACAGGTA 1


RESULT 6
AR180445
LOCUS       AR180445                  15 bp    DNA     linear   PAT 20-APR-2002
DEFINITION  Sequence 513 from patent US 6333152.
ACCESSION   AR180445
VERSION     AR180445.1  GI:20222478
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Vogelstein,B., Kinzler,K.W., Zhang,L. and Zhou,W.
  TITLE     Gene expression profiles in normal and cancer cells
  JOURNAL   Patent: US 6333152-A 513 25-DEC-2001;
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match            54.0%;  Score 10.8;  DB 1;  Length 15;
  Best Local Similarity  85.7%;  Pred. No. 6.8;
  Matches   12;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          4 CATGGTCACATGGA 17
              ||||| ||| ||||
Db          1 CATGGCCACGTGGA 14


RESULT 7
A71522
LOCUS       A71522                    12 bp    DNA     linear   PAT 07-MAY-1999
DEFINITION  Sequence 81 from Patent WO9813521.
ACCESSION   A71522
VERSION     A71522.1  GI:4775134
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified sequences.
REFERENCE   1  (bases 1 to 12)
  AUTHORS   Fesce,R. and Consalez,G.
  TITLE     METHOD FOR THE DIFFERENTIAL SCREENING OF GENE EXPRESSION BY RANDOM
            PRIMED REVERSE TRANSCRIPTION-POLYMERASE CHAIN REACTION
  JOURNAL   Patent: WO 9813521-A 81 02-APR-1998;
            FESCE RICCARDO (IT)
FEATURES             Location/Qualifiers
     source          1. .12
                     /organism="unidentified"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32644"

  Query Match            47.0%;  Score 9.4;  DB 1;  Length 12;
```

```
  Best Local Similarity   90.9%;  Pred. No. 8.2;
  Matches   10;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          6 TGGTCACATGG 16
              ||||||| |||
Db          2 TGGTCACGTGG 12


RESULT 8
S74610
LOCUS       S74610                    12 bp    mRNA    linear   PRI 07-MAY-1993
DEFINITION  lipoprotein lipase (exon 2-exon 3 boundary) [human, mRNA Partial
            Mutant, 12 nt].
ACCESSION   S74610
VERSION     S74610.1  GI:241423
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 12)
  AUTHORS   Gotoda,T., Yamada,N., Murase,T., Inaba,T., Ishibashi,S.,
            Shimano,H., Koga,S., Yazaki,Y., Furuichi,Y. and Takaku,F.
  TITLE     Occurrence of multiple aberrantly spliced mRNAs upon a donor splice
            site mutation that causes familial lipoprotein lipase deficiency
  JOURNAL   J. Biol. Chem. 266 (36), 24757-24762 (1991)
   PUBMED   1761570
  REMARK    GenBank staff at the National Library of Medicine created this
            entry [NCBI gibbsq 74610] from the original journal article.
FEATURES             Location/Qualifiers
     source          1. .12
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
     gene            1. .12
                     /gene="lipoprotein lipase, LPL"
     CDS             1. .12
                     /gene="lipoprotein lipase, LPL"
                     /note="contains in-frame 18-base pair deletion; LPL"
                     /codon_start=1
                     /product="lipoprotein lipase"
                     /protein_id="AAB20748.1"
                     /db_xref="GI:241424"
                     /translation="FMVT"

  Query Match             47.0%;  Score 9.4;  DB 1;  Length 12;
  Best Local Similarity   90.9%;  Pred. No. 8.2;
  Matches   10;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 TCATGGTCACA 13
              ||||||| |||
Db          2 TCATGGTAACA 12


RESULT 9
AR759769
LOCUS       AR759769                  13 bp    DNA     linear   PAT 08-DEC-2005
DEFINITION  Sequence 12 from patent US 6958240.
ACCESSION   AR759769
VERSION     AR759769.1  GI:83326505
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Baird,E.E. and Dervan,P.B.
  TITLE     Inhibition of major groove DNA binding proteins by modified
            polyamides
  JOURNAL   Patent: US 6958240-A 12 25-OCT-2005;
            California Instiute of Technology; Pasadena, CA
FEATURES             Location/Qualifiers
     source          1. .13
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             47.0%;  Score 9.4;  DB 1;  Length 13;
  Best Local Similarity   90.9%;  Pred. No. 9.8;
  Matches   10;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 TCATGGTCACA 13
              ||||||||| |
Db          3 TCATGGTCATA 13


RESULT 10
AR759770/c
LOCUS       AR759770                  13 bp    DNA     linear   PAT 08-DEC-2005
DEFINITION  Sequence 13 from patent US 6958240.
ACCESSION   AR759770
VERSION     AR759770.1  GI:83326506
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Baird,E.E. and Dervan,P.B.
  TITLE     Inhibition of major groove DNA binding proteins by modified
            polyamides
  JOURNAL   Patent: US 6958240-A 13 25-OCT-2005;
            California Instiute of Technology; Pasadena, CA
FEATURES             Location/Qualifiers
     source          1. .13
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             47.0%;  Score 9.4;  DB 1;  Length 13;
  Best Local Similarity   90.9%;  Pred. No. 9.8;
  Matches   10;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 TCATGGTCACA 13
              ||||||||| |
Db         11 TCATGGTCATA 1


RESULT 11
AR058623/c
LOCUS       AR058623                  12 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 200 from patent US 5837832.
ACCESSION   AR058623
VERSION     AR058623.1  GI:5984200
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 12)
  AUTHORS   Chee,M., Cronin,M.T., Fodor,S.P.A., Huang,X.X., Hubbell,E.A.,
            Lipshutz,R.J., Lobban,P.E., Morris,M.S. and Sheldon,E.L.
  TITLE     Arrays of nucleic acid probes on biological chips
  JOURNAL   Patent: US 5837832-A 200 17-NOV-1998;
FEATURES             Location/Qualifiers
     source          1. .12
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             45.0%;  Score 9;  DB 1;  Length 12;
  Best Local Similarity   100.0%;  Pred. No. 10;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 CATGGATGA 20
              |||||||||
Db         11 CATGGATGA 3


RESULT 12
I04322
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```
LOCUS       I04322                  12 bp    DNA     linear   PAT 02-DEC-1994
DEFINITION  Sequence 7 from Patent EP 0147819.
ACCESSION   I04322
VERSION     I04322.1  GI:591774
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 12)
  AUTHORS   Kung,H.-F. and Yamazaki,S.
  TITLE     Purification of recombinant interleukin-2
  JOURNAL   Patent: EP 0147819-A2 7 10-JUL-1985;
FEATURES             Location/Qualifiers
     source          1. .12
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             44.0%;  Score 8.8;  DB 1;  Length 12;
  Best Local Similarity   83.3%;  Pred. No. 11;
  Matches   10;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          6 TGGTCACATGGA 17
              | ||||| ||||
Db          1 TTGTCACGTGGA 12


RESULT 13
AR024074/c
LOCUS       AR024074                12 bp    DNA     linear   PAT 05-DEC-1998
DEFINITION  Sequence 24 from patent US 5795778.
ACCESSION   AR024074
VERSION     AR024074.1  GI:3977368
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 12)
  AUTHORS   Draper,K.G.
  TITLE     Method and reagent for inhibiting herpes simplex virus replication
  JOURNAL   Patent: US 5795778-A 24 18-AUG-1998;
FEATURES             Location/Qualifiers
     source          1. .12
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 12;
  Best Local Similarity   90.0%;  Pred. No. 13;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 TCATGGTCAC 12
              |||||| |||
Db         12 TCATGGCCAC 3


RESULT 14
AR075457/c
LOCUS       AR075457                12 bp    DNA     linear   PAT 30-AUG-2000
DEFINITION  Sequence 10 from patent US 5958424.
ACCESSION   AR075457
VERSION     AR075457.1  GI:10002207
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 12)
  AUTHORS   Noteborn,M.H.M. and De Boer,G.F.
  TITLE     Recombinant chicken anemia virus particle
  JOURNAL   Patent: US 5958424-A 10 28-SEP-1999;
FEATURES             Location/Qualifiers
     source          1. .12
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 12;
  Best Local Similarity   90.0%;  Pred. No. 13;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          7 GGTCACATGG 16
              |||||| |||
Db         12 GGTCACGTGG 3


RESULT 15
AR108947/c
LOCUS       AR108947                12 bp    DNA     linear   PAT 14-FEB-2001
DEFINITION  Sequence 2 from patent US 6113913.
ACCESSION   AR108947
VERSION     AR108947.1  GI:12825223
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 12)
  AUTHORS   Brough,D.E. and Kovesdi,I.
  TITLE     Recombinant adenovirus
  JOURNAL   Patent: US 6113913-A 2 05-SEP-2000;
FEATURES             Location/Qualifiers
     source          1. .12
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 12;
  Best Local Similarity   90.0%;  Pred. No. 13;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          7 GGTCACATGG 16
              |||||| |||
Db         12 GGTCACGTGG 3


RESULT 16
AR153908/c
LOCUS       AR153908                12 bp    DNA     linear   PAT 08-AUG-2001
DEFINITION  Sequence 10 from patent US 6238669.
ACCESSION   AR153908
VERSION     AR153908.1  GI:15121961
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 12)
  AUTHORS   Noteborn,M.H.M. and De Boer,G.F.
  TITLE     Proteins encoded by chicken anemia virus DNA and diagnostic kits
            and vaccines employing said proteins
  JOURNAL   Patent: US 6238669-A 10 29-MAY-2001;
FEATURES             Location/Qualifiers
     source          1. .12
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 12;
  Best Local Similarity   90.0%;  Pred. No. 13;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          7 GGTCACATGG 16
              |||||| |||
Db         12 GGTCACGTGG 3


RESULT 17
AR172244/c
LOCUS       AR172244                12 bp    DNA     linear   PAT 17-DEC-2001
DEFINITION  Sequence 68 from patent US 6303295.
ACCESSION   AR172244
VERSION     AR172244.1  GI:17911735
KEYWORDS    .
```

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SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 12)
  AUTHORS   Taylor,E.Will., Nadimpalli,R.Gopal. and Ramanathan,C.Sekar.
  TITLE     Selenoproteins, coding sequences and methods
  JOURNAL   Patent: US 6303295-A 68 16-OCT-2001;
FEATURES             Location/Qualifiers
     source          1. .12
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match           42.0%;  Score 8.4;  DB 1;  Length 12;
  Best Local Similarity   90.0%;  Pred. No. 13;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 CTCATGGTCA 11
              |||| |||||
Db         11 CTCAGGGTCA 2


RESULT 18
AR178525/c
LOCUS       AR178525                12 bp    DNA     linear   PAT 20-APR-2002
DEFINITION  Sequence 10 from patent US 6319693.
ACCESSION   AR178525
VERSION     AR178525.1  GI:20219663
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 12)
  AUTHORS   Noteborn,M.H.M. and de Boer,G.F.
  TITLE     Cloning of chicken anemia virus DNA
  JOURNAL   Patent: US 6319693-A 10 20-NOV-2001;
FEATURES             Location/Qualifiers
     source          1. .12
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match           42.0%;  Score 8.4;  DB 1;  Length 12;
  Best Local Similarity   90.0%;  Pred. No. 13;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          7 GGTCACATGG 16
              |||||| |||
Db         12 GGTCACGTGG 3


RESULT 19
BD001178/c
LOCUS       BD001178                12 bp    RNA     linear   PAT 31-JAN-2002
DEFINITION  Method and reagent for inhibiting viral replication.
ACCESSION   BD001178
VERSION     BD001178.1  GI:18625737
KEYWORDS    JP 2000342285-A/338.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 12)
  AUTHORS   Draper,K.G., Dadyktz,L.W., Macswigen,J.A., Maysejak,D.G.,
            Holesek,J.J. and Mamone,A.J.
  TITLE     Method and reagent for inhibiting viral replication
  JOURNAL   Patent: JP 2000342285-A 338 12-DEC-2000;
            RIBOZYME PHARMACEUTICALS INC
COMMENT     OS   Artificial Sequence
            PN   JP 2000342285-A/338
            PD   12-DEC-2000
            PF   01-MAY-2000 JP 2000132616
            PR   11-MAY-1992 US    07/882689,14-MAY-1992 US    07/882712 PR
            14-MAY-1992 US    07/882713,14-MAY-1992 US    07/882714 PR
            14-MAY-1992 US    07/882823,14-MAY-1992 US    07/882824 PR
            14-MAY-1992 US    07/882886,14-MAY-1992 US    07/882888 PR
            14-MAY-1992 US    07/882889,14-MAY-1992 US    07/882921 PR
            14-MAY-1992 US    07/882922,14-MAY-1992 US    07/883823 PR
            14-MAY-1992 US    07/883849,14-MAY-1992 US    07/884073 PR
            14-MAY-1992 US    07/884074,14-MAY-1992 US    07/884333 PR
            14-MAY-1992 US    07/884422,14-MAY-1992 US    07/884431 PR
            14-MAY-1992 US    07/884436,14-MAY-1992 US    07/884521 PR
            31-JUL-1992 US    07/923738,26-AUG-1992 US    07/935854 PR
            26-AUG-1992 US    07/936086,18-SEP-1992 US    07/948359 PR
            15-OCT-1992 US    07/963322,07-DEC-1992 US    07/987129 PR
            07-DEC-1992 US    07/987130,07-DEC-1992 US    07/987133 PI
            KENNETH G DRAPER,LEC W DADYKTZ,JAMES A MACSWIGEN, PI   DENNIS G
            MAYSEJAK,
            PI   JAMES J HOLESEK,ANTHONY J MAMONE
            PC   C12N15/09,C12N5/10,C12N7/00,C12N9/22//(C12N5/10,C12R1:91), PC
             C12N15/00,
            PC   C12N5/00,(C12N5/00,C12R1:91)
            CC
            FH   Key             Location/Qualifiers
            FT   source          1. .12
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .12
                     /organism="synthetic construct"
                     /mol_type="genomic RNA"
                     /db_xref="taxon:32630"

  Query Match           42.0%;  Score 8.4;  DB 1;  Length 12;
  Best Local Similarity   90.0%;  Pred. No. 13;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 TCATGGTCAC 12
              |||||| |||
Db         12 TCATGGCCAC 3


RESULT 20
BD001607/c
LOCUS       BD001607                12 bp    RNA     linear   PAT 31-JAN-2002
DEFINITION  Method and reagent for inhibiting viral replication.
ACCESSION   BD001607
VERSION     BD001607.1  GI:18626166
KEYWORDS    JP 2000342286-A/338.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 12)
  AUTHORS   Draper,K.G., Dadyktz,L.W., Macswigen,J.A., Maysejak,D.G.,
            Holesek,J.J. and Mamone,A.J.
  TITLE     Method and reagent for inhibiting viral replication
  JOURNAL   Patent: JP 2000342286-A 338 12-DEC-2000;
            RIBOZYME PHARMACEUTICALS INC
COMMENT     OS   Artificial Sequence
            PN   JP 2000342286-A/338
            PD   12-DEC-2000
            PF   01-MAY-2000 JP 2000132651
            PR   11-MAY-1992 US    07/882689,14-MAY-1992 US    07/882712 PR
            14-MAY-1992 US    07/882713,14-MAY-1992 US    07/882714 PR
            14-MAY-1992 US    07/882823,14-MAY-1992 US    07/882824 PR
            14-MAY-1992 US    07/882886,14-MAY-1992 US    07/882888 PR
            14-MAY-1992 US    07/882889,14-MAY-1992 US    07/882921 PR
            14-MAY-1992 US    07/882922,14-MAY-1992 US    07/883823 PR
            14-MAY-1992 US    07/883849,14-MAY-1992 US    07/884073 PR
            14-MAY-1992 US    07/884074,14-MAY-1992 US    07/884333 PR
            14-MAY-1992 US    07/884422,14-MAY-1992 US    07/884431 PR
            14-MAY-1992 US    07/884436,14-MAY-1992 US    07/884521 PR
            31-JUL-1992 US    07/923738,26-AUG-1992 US    07/935854 PR
            26-AUG-1992 US    07/936086,18-SEP-1992 US    07/948359 PR
            15-OCT-1992 US    07/963322,07-DEC-1992 US    07/987129 PR
            07-DEC-1992 US    07/987130,07-DEC-1992 US    07/987133 PI
            KENNETH G DRAPER,LEC W DADYKTZ,JAMES A MACSWIGEN, PI   DENNIS G
            MAYSEJAK,
            PI   JAMES J HOLESEK,ANTHONY J MAMONE
            PC   C12N15/09,C12N5/10,C12N7/00//A61K38/43,A61K39/125,A61K39/13,
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            PC   A61K39/135,
            PC   A61K39/145,A61K39/21,A61K39/23,A61K39/245,A61K39/29,A61K48/00,
            PC   A61P1/16,
            PC   A61P31/14,A61P31/16,A61P31/18,A61P31/22,A61P35/02,C12Q1/68, PC
              (C12N15/09,C12R1:93),C12N15/00,C12N5/00,A61K37/48,(C12N15/00, PC
             C12R1:93)
            CC
            FH   Key             Location/Qualifiers
            FT   source          1. .12
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .12
                     /organism="synthetic construct"
                     /mol_type="genomic RNA"
                     /db_xref="taxon:32630"

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 12;
  Best Local Similarity   90.0%;  Pred. No. 13;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 TCATGGTCAC 12
              |||||| |||
Db         12 TCATGGCCAC 3


RESULT 21
BD064941/c
LOCUS       BD064941                  12 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Method for detecting the extent of binding of transcriptional
            regulatory protein to oligoDNA.
ACCESSION   BD064941
VERSION     BD064941.1  GI:22610544
KEYWORDS    JP 2001275678-A/153.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 12)
  AUTHORS   Kishimoto,T., Niwa,S., Mori,Y., Sachiyo, Mimaki, Fukushima,R. and
            Nishikawa,K.
  TITLE     Method for detecting the extent of binding of transcriptional
            regulatory protein to oligoDNA
  JOURNAL   Patent: JP 2001275678-A 153 09-OCT-2001;
            SUMITOMO ELECTRIC INDUSTRIES LTD
COMMENT     OS   Artificial Sequence
            PN   JP 2001275678-A/153
            PD   09-OCT-2001
            PF   31-MAR-2000 JP 2000096306
            PI   TOSHIHIKO KISHIMOTO,SHINICHIRO NIWA,YUKO MORI,SACHIYO PI
            MIMAKI,REI FUKUSHIMA,
            PI   KAZUKO NISHIKAWA
            PC   C12N15/09,C12N5/10,C12Q1/00,C12Q1/68,C12N15/00,C12N5/00 CC
            Synthetic DNA
            FH   Key             Location/Qualifiers
            FT   source          1. .12
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .12
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 12;
  Best Local Similarity   90.0%;  Pred. No. 13;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          7 GGTCACATGG 16
              |||||| |||
Db         12 GGTCACGTGG 3


RESULT 22
BD240723/c
LOCUS       BD240723                  12 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Replication-deficient recombinant adenovirus having mutation major
            late promoter.
ACCESSION   BD240723
VERSION     BD240723.1  GI:33050493
KEYWORDS    JP 2002519036-A/2.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified sequences.
REFERENCE   1  (bases 1 to 12)
  AUTHORS   Brough,D.E. and Kovesdi,I.
  TITLE     Replication-deficient recombinant adenovirus having mutation major
            late promoter
  JOURNAL   Patent: JP 2002519036-A 2 02-JUL-2002;
            GENVEC INC
COMMENT     OS   Human adenovirus serotype 5
            PN   JP 2002519036-A/2
            PD   02-JUL-2002
            PF   24-JUN-1999 JP 2000557381
            PR   26-JUN-1998 US    09/105515
            PI   DOUGLAS E BROUGH,IMRE KOVESDI
            PC   C12N15/09,C12N5/10,C12N7/00//A61K35/76,A61K39/235,A61K48/00,
            PC   C12N15/00,
            PC   C12N5/00
            CC   Replication-deficient recombinant adenovirus having mutation
            CC            major late
            CC   promoter
            FH   Key             Location/Qualifiers
            FT   source          1. .12
            FT                   /organism='Human adenovirus serotype 5'.
FEATURES             Location/Qualifiers
     source          1. .12
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 12;
  Best Local Similarity   90.0%;  Pred. No. 13;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          7 GGTCACATGG 16
              |||||| |||
Db         12 GGTCACGTGG 3


RESULT 23
BD261806
LOCUS       BD261806                  12 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Enhancement in protein production by higher plants using ubiquitin
            or cucumber mosaic virus coating protein peptide.
ACCESSION   BD261806
VERSION     BD261806.1  GI:33071574
KEYWORDS    JP 2002532098-A/10.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified sequences.
REFERENCE   1  (bases 1 to 12)
  AUTHORS   Fang,R.X., Wu,J.L. and Chen,X.Y.
  TITLE     Enhancement in protein production by higher plants using ubiquitin
            or cucumber mosaic virus coating protein peptide
  JOURNAL   Patent: JP 2002532098-A 10 02-OCT-2002;
            INSTITUTE OF MOLECULAR AGROBIOLOGY
COMMENT     OS   Plasmid pCL
            PN   JP 2002532098-A/10
            PD   02-OCT-2002
            PF   11-DEC-1998 JP 2000588378
            PI   RONG XIANG FANG,JUNG LIN WU,XIAO YING CHEN
            PC   C12N15/09,A01H5/00,C07K14/415,C07K19/00,C12N5/10,C12N15/00, PC
              C12N5/00
            CC   Joining region between fusion of genes.
            FH   Key             Location/Qualifiers
            FT   misc_feature    (1). .(12).
FEATURES             Location/Qualifiers
     source          1. .12
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                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 12;
  Best Local Similarity   90.0%;  Pred. No. 13;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          8 GTCACATGGA 17
              ||| ||||||
Db          2 GTCGCATGGA 11


RESULT 24
CQ828540
LOCUS       CQ828540                  12 bp    DNA     linear   PAT 05-JUL-2004
DEFINITION  Sequence 258 from Patent WO2004053120.
ACCESSION   CQ828540
VERSION     CQ828540.1  GI:49732023
KEYWORDS    .
SOURCE      Rattus norvegicus (Norway rat)
  ORGANISM  Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Rattus.
REFERENCE   1
  AUTHORS   Weihe,E., Bieller,A. and Schaefer,M.K.
  TITLE     Regulatory elements in the 5' region of the vr1 gene
  JOURNAL   Patent: WO 2004053120-A 258 24-JUN-2004;
            Gruenenthal GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .12
                     /organism="Rattus norvegicus"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:10116"
                     /note="V$IK2 01"

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 12;
  Best Local Similarity   90.0%;  Pred. No. 13;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         10 CACATGGATG 19
              |||| |||||
Db          1 CACAGGGATG 10


RESULT 25
I17542/c
LOCUS       I17542                    12 bp    DNA     linear   PAT 07-OCT-1996
DEFINITION  Sequence 10 from patent US 5491073.
ACCESSION   I17542
VERSION     I17542.1  GI:1597897
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 12)
  AUTHORS   Noteborn,M.H.M. and de Boer,G.F.
  TITLE     Cloning of chicken anaemia DNA
  JOURNAL   Patent: US 5491073-A 10 13-FEB-1996;
FEATURES             Location/Qualifiers
     source          1. .12
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 12;
  Best Local Similarity   90.0%;  Pred. No. 13;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          7 GGTCACATGG 16
              |||||| |||
Db         12 GGTCACGTGG 3


RESULT 26
AR224293/c
LOCUS       AR224293                  12 bp    DNA     linear   PAT 26-SEP-2002
DEFINITION  Sequence 24 from patent US 6440719.
ACCESSION   AR224293
VERSION     AR224293.1  GI:23333070
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 12)
  AUTHORS   Draper,K.G.
  TITLE     Method and reagent for inhibiting herpes simplex virus replication
  JOURNAL   Patent: US 6440719-A 24 27-AUG-2002;
            Ribozyme Pharmaceuticals, Inc.; Boulder, CO
FEATURES             Location/Qualifiers
     source          1. .12
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 12;
  Best Local Similarity   90.0%;  Pred. No. 13;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 TCATGGTCAC 12
              |||||| |||
Db         12 TCATGGCCAC 3


RESULT 27
AR234464/c
LOCUS       AR234464                  12 bp    DNA     linear   PAT 20-DEC-2002
DEFINITION  Sequence 2 from patent US 6458578.
ACCESSION   AR234464
VERSION     AR234464.1  GI:27277166
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 12)
  AUTHORS   Brough,D.E. and Kovesdi,I.
  TITLE     Recombinant cell line produces adenoviral gene products E1 and
            DEF-A, and/or DEF-B
  JOURNAL   Patent: US 6458578-A 2 01-OCT-2002;
            GenVec, Inc.; Gaithersburg, MD
FEATURES             Location/Qualifiers
     source          1. .12
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 12;
  Best Local Similarity   90.0%;  Pred. No. 13;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          7 GGTCACATGG 16
              |||||| |||
Db         12 GGTCACGTGG 3


RESULT 28
AR275829/c
LOCUS       AR275829                  12 bp    DNA     linear   PAT 10-APR-2003
DEFINITION  Sequence 10 from patent US 6509446.
ACCESSION   AR275829
VERSION     AR275829.1  GI:29709474
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 12)
  AUTHORS   Noteborn,M.H.M. and De Boer,G.F.
  TITLE     Cloning of chicken anemia DNA
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  JOURNAL   Patent: US 6509446-A 10 21-JAN-2003;
            Leadd B.V.; Leiden;
            NLX;
FEATURES             Location/Qualifiers
     source          1. .12
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 12;
  Best Local Similarity   90.0%;  Pred. No. 13;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          7 GGTCACATGG 16
              |||||| |||
Db         12 GGTCACGTGG 3


RESULT 29
I58612/c
LOCUS       I58612                  12 bp    DNA     linear   PAT 07-OCT-1997
DEFINITION  Sequence 3 from patent US 5652144.
ACCESSION   I58612
VERSION     I58612.1  GI:2477850
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 12)
  AUTHORS   Lu,Y. and Haseltine,W.A.
  TITLE     YC1 gene
  JOURNAL   Patent: US 5652144-A 3 29-JUL-1997;
FEATURES             Location/Qualifiers
     source          1. .12
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 12;
  Best Local Similarity   90.0%;  Pred. No. 13;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          7 GGTCACATGG 16
              |||||| |||
Db         12 GGTCACGTGG 3


RESULT 30
I72395/c
LOCUS       I72395                  12 bp    DNA     linear   PAT 03-APR-1998
DEFINITION  Sequence 26 from patent US 5683985.
ACCESSION   I72395
VERSION     I72395.1  GI:3008534
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 12)
  AUTHORS   Chu,B.Chen.Fei. and Orgel,L.
  TITLE     Oligonucleotide decoys and methods relating thereto
  JOURNAL   Patent: US 5683985-A 26 04-NOV-1997;
FEATURES             Location/Qualifiers
     source          1. .12
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 12;
  Best Local Similarity   90.0%;  Pred. No. 13;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          7 GGTCACATGG 16
              |||||| |||
Db         12 GGTCACGTGG 3


RESULT 31
AR577337
LOCUS       AR577337                12 bp    DNA     linear   PAT 14-DEC-2004
DEFINITION  Sequence 54 from patent US 6777544.
ACCESSION   AR577337
VERSION     AR577337.1  GI:56579871
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 12)
  AUTHORS   Uhlmann,E., Breipohl,G. and Will,D.W.
  TITLE     Polyamide nucleic acid derivatives and agents and processes for
            preparing them
  JOURNAL   Patent: US 6777544-A 54 17-AUG-2004;
            Aventis Pharma Deutschland GmbH; Frankfurt;
            DEX;
FEATURES             Location/Qualifiers
     source          1. .12
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 12;
  Best Local Similarity   90.0%;  Pred. No. 13;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 CCTCATGGTC 10
              | ||||||||
Db          2 CATCATGGTC 11


RESULT 32
AR699868
LOCUS       AR699868                12 bp    DNA     linear   PAT 14-SEP-2005
DEFINITION  Sequence 38 from patent US 6919441.
ACCESSION   AR699868
VERSION     AR699868.1  GI:75205772
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 12)
  AUTHORS   Uhlmann,E. and Breipohl,G.
  TITLE     Polyamide-oligonucleotide derivatives, their preparation and use
  JOURNAL   Patent: US 6919441-A 38 19-JUL-2005;
            Aventis Pharma Deutschland GmbH; Frankfurt;
            DEX;
FEATURES             Location/Qualifiers
     source          1. .12
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 12;
  Best Local Similarity   90.0%;  Pred. No. 13;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 CCTCATGGTC 10
              | ||||||||
Db          2 CATCATGGTC 11


RESULT 33
AR699877
LOCUS       AR699877                12 bp    DNA     linear   PAT 14-SEP-2005
DEFINITION  Sequence 48 from patent US 6919441.
ACCESSION   AR699877
VERSION     AR699877.1  GI:75205785
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 12)
  AUTHORS   Uhlmann,E. and Breipohl,G.
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  TITLE     Polyamide-oligonucleotide derivatives, their preparation and use
  JOURNAL   Patent: US 6919441-A 48 19-JUL-2005;
            Aventis Pharma Deutschland GmbH; Frankfurt;
            DEX;
FEATURES             Location/Qualifiers
     source          1. .12
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match           42.0%;  Score 8.4;  DB 1;  Length 12;
  Best Local Similarity   90.0%;  Pred. No. 13;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 CCTCATGGTC 10
              | ||||||||
Db          2 CATCATGGTC 11


RESULT 34
AR699878/c
LOCUS       AR699878                 12 bp    DNA     linear   PAT 14-SEP-2005
DEFINITION  Sequence 49 from patent US 6919441.
ACCESSION   AR699878
VERSION     AR699878.1  GI:75205786
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 12)
  AUTHORS   Uhlmann,E. and Breipohl,G.
  TITLE     Polyamide-oligonucleotide derivatives, their preparation and use
  JOURNAL   Patent: US 6919441-A 49 19-JUL-2005;
            Aventis Pharma Deutschland GmbH; Frankfurt;
            DEX;
FEATURES             Location/Qualifiers
     source          1. .12
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match           42.0%;  Score 8.4;  DB 1;  Length 12;
  Best Local Similarity   90.0%;  Pred. No. 13;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 CCTCATGGTC 10
              | ||||||||
Db         11 CATCATGGTC 2


RESULT 35
AX283286
LOCUS       AX283286                 12 bp    DNA     linear   PAT 20-NOV-2001
DEFINITION  Sequence 50 from Patent WO0179249.
ACCESSION   AX283286
VERSION     AX283286.1  GI:17044167
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Uhlmann,E., Breipohl,G. and Will,D.W.
  TITLE     Polyamide nucleic acid derivatives, agents and methods for
            producing the same
  JOURNAL   Patent: WO 0179249-A 50 25-OCT-2001;
            Aventis Pharma Deutschland GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .12
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Beschreibung der kuenstlichen Sequenz:
                     Oligonukleotide"

  Query Match           42.0%;  Score 8.4;  DB 1;  Length 12;
  Best Local Similarity   90.0%;  Pred. No. 13;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 CCTCATGGTC 10
              | ||||||||
Db          2 CATCATGGTC 11


RESULT 36
AX711060/c
LOCUS       AX711060                 12 bp    RNA     linear   PAT 11-APR-2003
DEFINITION  Sequence 360 from Patent EP1288296.
ACCESSION   AX711060
VERSION     AX711060.1  GI:29787441
KEYWORDS    .
SOURCE      Herpes simplex virus unknown type
  ORGANISM  Herpes simplex virus unknown type
            Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
            Alphaherpesvirinae; Simplexvirus; unclassified Simplexvirus.
REFERENCE   1
  AUTHORS   Draper,K.G., Mcswiggen,J.A., Holecek,J.J., Dudycz,L.W.,
            Macejak,D.G. and Mamone,J.A.
  TITLE     Method and reagent for inhibiting HBV viral replication
  JOURNAL   Patent: EP 1288296-A 360 05-MAR-2003;
            RIBOZYME PHARMACEUTICALS, INC. (US)
FEATURES             Location/Qualifiers
     source          1. .12
                     /organism="Herpes simplex virus unknown type"
                     /mol_type="unassigned RNA"
                     /db_xref="taxon:126283"

  Query Match           42.0%;  Score 8.4;  DB 1;  Length 12;
  Best Local Similarity   90.0%;  Pred. No. 13;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 TCATGGTCAC 12
              |||||| |||
Db         12 TCATGGCCAC 3


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Job time : 0.001 secs
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